



SEQUENCE LISTING

<110> JAPAN SCIENCE AND TECHNOLOGY CORPORATION

<120> Screening of genes to give tolerance against
environmental stress and the applications

<130> YG12-12PCT

<140>

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<150> JP P1999-235910

<151> 1999-07-19

<150> JP P2000-85377

<151> 2000-03-24

<160> 72

<170> PatentIn Ver. 2.1

<210> 1

<211> 1018

<212> DNA

<213> Bruguiera sexangula

<220>

<221> CDS

<222> (42)..(464)

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Met Ala Leu Ser Ser

tct gct ctg aga acc gtc tct tct tct gtg aag gtg gtc ggc cct gca 104
 Ser Ala Leu Arg Thr Val Ser Ser Ser Val Lys Val Val Gly Pro Ala

10 15 20

aga tca aag agt gct act gta ccc acc caa aca gta ttg cct ttc aag 152
 Arg Ser Lys Ser Ala Thr Val Pro Thr Gln Thr Val Leu Pro Phe Lys

25 30 35

ttc aca aac ccg tcg tta ctc act cga tcg cta agc ttt tca tca aaa 200
 Phe Thr Asn Pro Ser Leu Leu Thr Arg Ser Leu Ser Phe Ser Ser Lys

40 45 50

ggt tca agc ttt gac agc ttc tct gta ccc aaa aga tct ttt tct tgc 248
 Gly Ser Ser Phe Asp Ser Phe Ser Val Pro Lys Arg Ser Phe Ser Cys

55 60 65

aga agc caa gcc act cca tct gat gat gcc tca aga ccc acc aaa gtt 296
 Arg Ser Gln Ala Thr Pro Ser Asp Asp Ala Ser Arg Pro Thr Lys Val

70 75 80 85

caa gag ctg tgt gtg tat gag atg aac gag aga gat cgt gga agc cct 344
 Gln Glu Leu Cys Val Tyr Glu Met Asn Glu Arg Asp Arg Gly Ser Pro

90 95 100

gct gtt ctc cgg ttg agc cag aaa cct gtt aat tct ctc ggc gat ctc 392
 Ala Val Leu Arg Leu Ser Gln Lys Pro Val Asn Ser Leu Gly Asp Leu

105 110 115

gtg cct ttc agt aac aaa gtt tac agc gga gac ctg cag aag cga att 440
 Val Pro Phe Ser Asn Lys Val Tyr Ser Gly Asp Leu Gln Lys Arg Ile

120 125 130

gga gta acc gca gaa tat gca tcc tgatccaaaa caagccagaa aaaaagggtg 494
 Gly Val Thr Ala Glu Tyr Ala Ser

135 140

atcgtttga agcgatatat agcttttatt tcggtggcta tggtcacatt gctgtgcaag 554
 gcgcatactt gacctacgag gacacgcacc ttgctgtgac gggcgggtcg ggcataattg 614
 aaggagtgtc tggtcagggtt aagctgcagc aactcgtgta ccctttcaag ctcttctaca 674
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 ctaatttcac cgattagtga ttaattgtcc ttttgggggt cggatgaact tgagttagct 854
 tacagttgca caacgttatg gcgcgagaca cgagagggaa ccttagccat aagaaaatta 914
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<210> 2

<211> 141

<212> PRT

<213> *Bruguiera sexangula*

<400> 2

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Val Val Gly Pro Ala Arg Ser Lys Ser Ala Thr Val Pro Thr Gln Thr

20 25 30

Val Leu Pro Phe Lys Phe Thr Asn Pro Ser Leu Leu Thr Arg Ser Leu

35 40 45

Ser Phe Ser Ser Lys Gly Ser Ser Phe Asp Ser Phe Ser Val Pro Lys

50 55 60

Arg Ser Phe Ser Cys Arg Ser Gln Ala Thr Pro Ser Asp Asp Ala Ser
65 70 75 80

Arg Pro Thr Lys Val Gln Glu Leu Cys Val Tyr Glu Met Asn Glu Arg
85 90 95

Asp Arg Gly Ser Pro Ala Val Leu Arg Leu Ser Gln Lys Pro Val Asn
100 105 110

Ser Leu Gly Asp Leu Val Pro Phe Ser Asn Lys Val Tyr Ser Gly Asp
115 120 125

Leu Gln Lys Arg Ile Gly Val Thr Ala Glu Tyr Ala Ser
130 135 140

<210> 3

<211> 2060

<212> DNA

<213> *Bruguiera sexangula*

<220>

<221> CDS

<222> (81)..(1718)

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ttctgtttct ttgaccagaa atg gca atc gcg gct caa act ccg gac att ctc 113

Met Ala Ile Ala Ala Gln Thr Pro Asp Ile Leu

1 5 10

ggc gaa cgt cag tcc ggc cag gac gtc cgc act caa aat gtg gtg gca 161

Gly Glu Arg Gln Ser Gly Gln Asp Val Arg Thr Gln Asn Val Val Ala

15	20	25	
tgt caa gcg gtt gcc aat att gtc aaa tct tca ctt ggt cct gtc gga			209
Cys Gln Ala Val Ala Asn Ile Val Lys Ser Ser Leu Gly Pro Val Gly			
30	35	40	
ctc gac aag atg cta gtg gat gat att ggt gat gta aca att aca aat			257
Leu Asp Lys Met Leu Val Asp Asp Ile Gly Asp Val Thr Ile Thr Asn			
45	50	55	
gat ggt gct acg att ctt aag atg tta gaa gta gag cat cct gca gca			305
Asp Gly Ala Thr Ile Leu Lys Met Leu Glu Val Glu His Pro Ala Ala			
60	65	70	75
aag gtg ctc gtg gag ttg gct gag ctt caa gac cga gaa gtt gga gat			353
Lys Val Leu Val Glu Leu Ala Glu Leu Gln Asp Arg Glu Val Gly Asp			
80	85	90	
gga acc act tcg gtt gtc atc ata gca gct gag ttg ctc aag aga gca			401
Gly Thr Thr Ser Val Val Ile Ile Ala Ala Glu Leu Leu Lys Arg Ala			
95	100	105	
aat gat ctc gtg agg aat aag atc cac cca aca tca ata atc agt gga			449
Asn Asp Leu Val Arg Asn Lys Ile His Pro Thr Ser Ile Ile Ser Gly			
110	115	120	
tac agg ctt gct atg agg gaa gca tgc aag tat gtt gaa gag aaa ttg			497
Tyr Arg Leu Ala Met Arg Glu Ala Cys Lys Tyr Val Glu Glu Lys Leu			
125	130	135	
tca atg aag gtt gaa aag ctt gga aaa gat tct cta gta aac tgt gca			545
Ser Met Lys Val Glu Lys Leu Gly Lys Asp Ser Leu Val Asn Cys Ala			
140	145	150	155
aag aca agc atg tcc tca aag ttg ata gct ggt gac agc gac ttc ttt			593
Lys Thr Ser Met Ser Ser Lys Leu Ile Ala Gly Asp Ser Asp Phe Phe			

160	165	170	
gca aat ttg gtt gta gat gct gta caa gca gta aag atg acc aat gca			641
Ala Asn Leu Val Val Asp Ala Val Gln Ala Val Lys Met Thr Asn Ala			
175	180	185	
cgg ggg gaa atc aaa tat cct atc aag agt ata aat att ttg aaa gct			689
Arg Gly Glu Ile Lys Tyr Pro Ile Lys Ser Ile Asn Ile Leu Lys Ala			
190	195	200	
cat gga aaa agt gca aga gat agc tgc ctt ttg aat ggc tat gct ctc			737
His Gly Lys Ser Ala Arg Asp Ser Cys Leu Leu Asn Gly Tyr Ala Leu			
205	210	215	
aat act ggt cgt gct gct caa ggg atg cct atg aga gtt gca cct gca			785
Asn Thr Gly Arg Ala Ala Gln Gly Met Pro Met Arg Val Ala Pro Ala			
220	225	230	235
agg att gct tgt ctt gac ttt aat ctt cag aaa acg aag atg caa ttg			833
Arg Ile Ala Cys Leu Asp Phe Asn Leu Gln Lys Thr Lys Met Gln Leu			
240	245	250	
ggc gta caa gtc tta gtc act gat ccc agg gag ctt gaa aga att cgt			881
Gly Val Gln Val Leu Val Thr Asp Pro Arg Glu Leu Glu Arg Ile Arg			
255	260	265	
caa aga gaa gct gat atg aca aag gaa cgg att gag aaa ctc ctg aaa			929
Gln Arg Glu Ala Asp Met Thr Lys Glu Arg Ile Glu Lys Leu Leu Lys			
270	275	280	
gct gga gca aat gtt gtt cta acc aca aag gga att gat gac atg gca			977
Ala Gly Ala Asn Val Val Leu Thr Thr Lys Gly Ile Asp Asp Met Ala			
285	290	295	
ctt aaa tat ttt gtg gag gct ggg gct att gct gtg aga cgt gtt cgg			1025
Leu Lys Tyr Phe Val Glu Ala Gly Ala Ile Ala Val Arg Arg Val Arg			

300	305	310	315	
aaa gag gat atg cgc cat gtt gcc aag gca act ggt gca aca ctg gtt				1073
Lys Glu Asp Met Arg His Val Ala Lys Ala Thr Gly Ala Thr Leu Val				
	320	325	330	
tca aca ttt gct gac atg gaa gga gag gaa aca ttt gat tca tca ctg				1121
Ser Thr Phe Ala Asp Met Glu Gly Glu Glu Thr Phe Asp Ser Ser Leu				
	335	340	345	
ctt gga caa gct gaa gaa gtt gtg gag gag cgc att gct gat gac gat				1169
Leu Gly Gln Ala Glu Glu Val Val Glu Glu Arg Ile Ala Asp Asp Asp				
	350	355	360	
gtg att atg ata aaa ggg aca aag act aca agt gcg gtt tcc ttg att				1217
Val Ile Met Ile Lys Gly Thr Lys Thr Thr Ser Ala Val Ser Leu Ile				
	365	370	375	
ctt cgt ggt gca aat gac tat atg ctc gat gag atg gag cga gcc ctg				1265
Leu Arg Gly Ala Asn Asp Tyr Met Leu Asp Glu Met Glu Arg Ala Leu				
380	385	390	395	
cat gat gct tta tgt att gtc aag aga acc ctt gaa tct aat aca gta				1313
His Asp Ala Leu Cys Ile Val Lys Arg Thr Leu Glu Ser Asn Thr Val				
	400	405	410	
gtt gca ggt gga ggt gct gtt gag gct gcc ttg tct gtg cac ttg gag				1361
Val Ala Gly Gly Gly Ala Val Glu Ala Ala Leu Ser Val His Leu Glu				
	415	420	425	
tac ctc gct aca act ctt ggg tca cga gag cag tta gca ata gca gag				1409
Tyr Leu Ala Thr Thr Leu Gly Ser Arg Glu Gln Leu Ala Ile Ala Glu				
	430	435	440	
ttt gca gaa tcc ttg ttg att ata cca aag gtt ctt gct gtc aat gct				1457
Phe Ala Glu Ser Leu Leu Ile Ile Pro Lys Val Leu Ala Val Asn Ala				

445	450	455	
gcc aaa gat gcc act gaa tta gct gca aaa ctc cgg gct tac cac cat			1505
Ala Lys Asp Ala Thr Glu Leu Ala Ala Lys Leu Arg Ala Tyr His His			
460	465	470	475
aca gca caa aca aag gct gat aag aaa cat tta tca agc atg gga cta			1553
Thr Ala Gln Thr Lys Ala Asp Lys Lys His Leu Ser Ser Met Gly Leu			
	480	485	490
gac ctt tca aag ggg acc atc cga aac aac tta gaa gct gga gtc att			1601
Asp Leu Ser Lys Gly Thr Ile Arg Asn Asn Leu Glu Ala Gly Val Ile			
	495	500	505
gaa cct gca atg agc aaa ata aag ata att cag ttt gct act gaa gca			1649
Glu Pro Ala Met Ser Lys Ile Lys Ile Ile Gln Phe Ala Thr Glu Ala			
	510	515	520
gcc ata aca att ctt cga att gat gac atg atc aag ctt gtc aag gat			1697
Ala Ile Thr Ile Leu Arg Ile Asp Asp Met Ile Lys Leu Val Lys Asp			
	525	530	535
gag act cag aat gaa gag gaa tagatgcaga ctcttgtaag ctgcctccct			1748
Glu Thr Gln Asn Glu Glu Glu			
540	545		
tttgttttca aatttgtgtc ccttgcgagc tggaggaaag ggggggtgtt tatgtggtgt			1808
tttcagtgggt tttaattttt caaggagctc ggggcctgtg tacttttaggt tagagtccat			1868
ccaaggggtg tttattggat aatgcctaag ctgtttctcg tctattagta ggctggtagt			1928
tccactgagt tctcatccca attaaaagaa tgagatcaaa gggctcctaaa ttcgtactca			1988
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aaaaaaaaaa aa

2060

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<211> 546

<212> PRT

<213> *Bruguiera sexangula*

<400> 4

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20 25 30

Asn Ile Val Lys Ser Ser Leu Gly Pro Val Gly Leu Asp Lys Met Leu
35 40 45

Val Asp Asp Ile Gly Asp Val Thr Ile Thr Asn Asp Gly Ala Thr Ile
50 55 60

Leu Lys Met Leu Glu Val Glu His Pro Ala Ala Lys Val Leu Val Glu
65 70 75 80

Leu Ala Glu Leu Gln Asp Arg Glu Val Gly Asp Gly Thr Thr Ser Val
85 90 95

Val Ile Ile Ala Ala Glu Leu Leu Lys Arg Ala Asn Asp Leu Val Arg
100 105 110

Asn Lys Ile His Pro Thr Ser Ile Ile Ser Gly Tyr Arg Leu Ala Met
115 120 125

Arg Glu Ala Cys Lys Tyr Val Glu Glu Lys Leu Ser Met Lys Val Glu
130 135 140

Lys Leu Gly Lys Asp Ser Leu Val Asn Cys Ala Lys Thr Ser Met Ser
145 150 155 160

Ser Lys Leu Ile Ala Gly Asp Ser Asp Phe Phe Ala Asn Leu Val Val
165 170 175

Asp Ala Val Gln Ala Val Lys Met Thr Asn Ala Arg Gly Glu Ile Lys
180 185 190

Tyr Pro Ile Lys Ser Ile Asn Ile Leu Lys Ala His Gly Lys Ser Ala
195 200 205

Arg Asp Ser Cys Leu Leu Asn Gly Tyr Ala Leu Asn Thr Gly Arg Ala
210 215 220

Ala Gln Gly Met Pro Met Arg Val Ala Pro Ala Arg Ile Ala Cys Leu
225 230 235 240

Asp Phe Asn Leu Gln Lys Thr Lys Met Gln Leu Gly Val Gln Val Leu
245 250 255

Val Thr Asp Pro Arg Glu Leu Glu Arg Ile Arg Gln Arg Glu Ala Asp
260 265 270

Met Thr Lys Glu Arg Ile Glu Lys Leu Leu Lys Ala Gly Ala Asn Val
275 280 285

Val Leu Thr Thr Lys Gly Ile Asp Asp Met Ala Leu Lys Tyr Phe Val
290 295 300

Glu Ala Gly Ala Ile Ala Val Arg Arg Val Arg Lys Glu Asp Met Arg
305 310 315 320

His Val Ala Lys Ala Thr Gly Ala Thr Leu Val Ser Thr Phe Ala Asp
325 330 335

Met Glu Gly Glu Glu Thr Phe Asp Ser Ser Leu Leu Gly Gln Ala Glu
340 345 350

Glu Val Val Glu Glu Arg Ile Ala Asp Asp Asp Val Ile Met Ile Lys
355 360 365

Gly Thr Lys Thr Thr Ser Ala Val Ser Leu Ile Leu Arg Gly Ala Asn
370 375 380

Asp Tyr Met Leu Asp Glu Met Glu Arg Ala Leu His Asp Ala Leu Cys
385 390 395 400

Ile Val Lys Arg Thr Leu Glu Ser Asn Thr Val Val Ala Gly Gly Gly
405 410 415

Ala Val Glu Ala Ala Leu Ser Val His Leu Glu Tyr Leu Ala Thr Thr
420 425 430

Leu Gly Ser Arg Glu Gln Leu Ala Ile Ala Glu Phe Ala Glu Ser Leu
435 440 445

Leu Ile Ile Pro Lys Val Leu Ala Val Asn Ala Ala Lys Asp Ala Thr
450 455 460

Glu Leu Ala Ala Lys Leu Arg Ala Tyr His His Thr Ala Gln Thr Lys
465 470 475 480

Ala Asp Lys Lys His Leu Ser Ser Met Gly Leu Asp Leu Ser Lys Gly
485 490 495

Thr Ile Arg Asn Asn Leu Glu Ala Gly Val Ile Glu Pro Ala Met Ser
500 505 510

Lys Ile Lys Ile Ile Gln Phe Ala Thr Glu Ala Ala Ile Thr Ile Leu
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Arg Ile Asp Asp Met Ile Lys Leu Val Lys Asp Glu Thr Gln Asn Glu
530 535 540

Glu Glu
545

<210> 5
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<212> DNA
<213> *Bruguiera sexangula*

<220>
<221> CDS
<222> (26).. (262)

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Met Ser Cys Cys Gly Gly Asn Cys Gly
1 5
tgc gga gca agc tgc aat tgc ggc aac ggc tgt gga ggg tgc aag atg 100
Cys Gly Ala Ser Cys Asn Cys Gly Asn Gly Cys Gly Gly Cys Lys Met
10 15 20 25
tac cca gac atg ggc ttc gcc gag aag acc act acc gag act ctg gtt 148
Tyr Pro Asp Met Gly Phe Ala Glu Lys Thr Thr Thr Glu Thr Leu Val
30 35 40
ctc ggc gtg ggg cct gag agg gcc cac ttt gag gga gcc gag atg ggc 196
Leu Gly Val Gly Pro Glu Arg Ala His Phe Glu Gly Ala Glu Met Gly
45 50 55
gtg ccg gcc gag aac gga ggc tgc aag tgc gga agt aac tgc acc tgc 244
Val Pro Ala Glu Asn Gly Gly Cys Lys Cys Gly Ser Asn Cys Thr Cys

60

65

70

gac ccc tgc act tgt aaa tgaggggaaa gtgacaggga aggtccgac 292

Asp Pro Cys Thr Cys Lys

75

tattattagt ctatatgtgt gtgttgggag tcttgcttac aataaaccag tcatgccttg 352

cgtttcctcc atgcgcagat cttaggtttt aggatatctc tgtggtttct ccaagctatg 412

gattttcagt gtctagtttt cctgtattac aaggatagtt tataaccgta tatgcatggt 472

cggaatcctt ccaaccattt cgtttgtcta aatatatata tgtgtgtgtg tgtgtgtgtt 532

tgatgggaaa gtgagcttct ttatgtttta tgactaaaaa aaaaaaaaaa aaaaaa 588

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<211> 79

<212> PRT

<213> *Bruguiera sexangula*

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1

5

10

15

Gly Asn Gly Cys Gly Gly Cys Lys Met Tyr Pro Asp Met Gly Phe Ala

20

25

30

Glu Lys Thr Thr Thr Glu Thr Leu Val Leu Gly Val Gly Pro Glu Arg

35

40

45

Ala His Phe Glu Gly Ala Glu Met Gly Val Pro Ala Glu Asn Gly Gly

50

55

60

Cys Lys Cys Gly Ser Asn Cys Thr Cys Asp Pro Cys Thr Cys Lys

75

<213> Bruguiera sexangula

 $\langle 222 \rangle$ (1) .. (1002)

1 5 10 15

20 25 30

35 40 45

50 55 60

65 70 75 80

Ala Met Gly Pro Gln Val Lys Phe Val Gln Cys Pro Asp Gly Glu Leu

85	90	95	
cag aag agg aaa gag gtc gtg cat tgt gtc tca ctg cac gag att gat			336
Gln Lys Arg Lys Glu Val Val His Cys Val Ser Leu His Glu Ile Asp			
100	105	110	
gtt atc aat agc aga aca cag ggg ttt ctt gct ctt ttc acc ggg gat			384
Val Ile Asn Ser Arg Thr Gln Gly Phe Leu Ala Leu Phe Thr Gly Asp			
115	120	125	
act ggt gaa atc cgt gcg gag gtg agg gaa caa att gac aca aag gtg			432
Thr Gly Glu Ile Arg Ala Glu Val Arg Glu Gln Ile Asp Thr Lys Val			
130	135	140	
gct gaa tgg aga gag gaa ggg aaa gca gag att gtg cca ggt gtc ctc			480
Ala Glu Trp Arg Glu Glu Gly Lys Ala Glu Ile Val Pro Gly Val Leu			
145	150	155	160
ttt att gat gag gtc cac atg ctt gac att gag tgc ttc tca ttt ctg			528
Phe Ile Asp Glu Val His Met Leu Asp Ile Glu Cys Phe Ser Phe Leu			
165	170	175	
aat cgt gct ctt gag aat gag atg gcg cca ata tta gtt gtt gct acc			576
Asn Arg Ala Leu Glu Asn Glu Met Ala Pro Ile Leu Val Val Ala Thr			
180	185	190	
aac aga ggg atc acc aca atc aga ggc aca aat tac aaa tct cct cat			624
Asn Arg Gly Ile Thr Thr Ile Arg Gly Thr Asn Tyr Lys Ser Pro His			
195	200	205	
ggg att cca ata gat ctc ctt gat cga cta ctc att atc aca act caa			672
Gly Ile Pro Ile Asp Leu Leu Asp Arg Leu Leu Ile Ile Thr Thr Gln			
210	215	220	
cct tac aca aag gat gaa att cgt aag att ctg gat atc aga tgt cag			720
Pro Tyr Thr Lys Asp Glu Ile Arg Lys Ile Leu Asp Ile Arg Cys Gln			

225	230	235	240	
gaa gaa gat gtg gag atg gct gaa gag gca aag gct ttg tta aca cat				768
Glu Glu Asp Val Glu Met Ala Glu Glu Ala Lys Ala Leu Leu Thr His				
	245	250	255	
att ggg gca gaa aca tcc ttg aga tat gcc atc cat ctc att act gct				816
Ile Gly Ala Glu Thr Ser Leu Arg Tyr Ala Ile His Leu Ile Thr Ala				
	260	265	270	
gca gca ttg gca tgc cag aag cga aag gga aag ctt gtg gaa act gag				864
Ala Ala Leu Ala Cys Gln Lys Arg Lys Gly Lys Leu Val Glu Thr Glu				
	275	280	285	
gac att agt cga gct tac aat ctg ttt ctt gat gta aag aga tct aca				912
Asp Ile Ser Arg Ala Tyr Asn Leu Phe Leu Asp Val Lys Arg Ser Thr				
	290	295	300	
cag tac cta ata gag tat cag aat cag tac atg ttt aat gag gca ccg				960
Gln Tyr Leu Ile Glu Tyr Gln Asn Gln Tyr Met Phe Asn Glu Ala Pro				
305	310	315	320	
gta gga gaa ggg gac gaa gaa ggg gcc aat gcc atg ctt tct				1002
Val Gly Glu Gly Asp Glu Glu Gly Ala Asn Ala Met Leu Ser				
	325	330		
tgaaggcca taagctatgg agtcctttgtg aaacccttct ccctacttta ttgcagcac				1062
gagccctgaa atgaagaaca atggtagact tggatccac cttggccctt atgtatgtct				1122
tctggaattg aaaaaagagt ccaagaaatt tgaatttcat gaaattggag aactgaactg				1182
tgcttactaa attgctactt tgcaagtaat gatagggcac tcacgcttga ctggctaagt				1242
atztatgttt ttatcatcaa aaaaaaaaaa aaaaaaaaaa				1280

<210> 8

<211> 334

<212> PRT

<213> Bruguiera sexangula

<400> 8

Ile Glu Gly Glu Val Val Glu Val Gln Ile Asp Arg Pro Ala Val Thr

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20 25 30

Glu Thr Val Tyr Asp Leu Gly Ala Lys Met Ile Glu Ala Leu Gly Lys

35 40 45

Glu Lys Val Gln Ser Gly Asp Val Ile Ala Ile Asp Lys Ala Ser Gly

50 55 60

Lys Ile Thr Lys Leu Gly Arg Ser Phe Ser Arg Ser Arg Asp Tyr Asp

65 70 75 80

Ala Met Gly Pro Gln Val Lys Phe Val Gln Cys Pro Asp Gly Glu Leu

85 90 95

Gln Lys Arg Lys Glu Val Val His Cys Val Ser Leu His Glu Ile Asp

100 105 110

Val Ile Asn Ser Arg Thr Gln Gly Phe Leu Ala Leu Phe Thr Gly Asp

115 120 125

Thr Gly Glu Ile Arg Ala Glu Val Arg Glu Gln Ile Asp Thr Lys Val

130 135 140

Ala Glu Trp Arg Glu Glu Gly Lys Ala Glu Ile Val Pro Gly Val Leu

145 150 155 160

Phe Ile Asp Glu Val His Met Leu Asp Ile Glu Cys Phe Ser Phe Leu
165 170 175

Asn Arg Ala Leu Glu Asn Glu Met Ala Pro Ile Leu Val Val Ala Thr
180 185 190

Asn Arg Gly Ile Thr Thr Ile Arg Gly Thr Asn Tyr Lys Ser Pro His
195 200 205

Gly Ile Pro Ile Asp Leu Leu Asp Arg Leu Leu Ile Ile Thr Thr Gln
210 215 220

Pro Tyr Thr Lys Asp Glu Ile Arg Lys Ile Leu Asp Ile Arg Cys Gln
225 230 235 240

Glu Glu Asp Val Glu Met Ala Glu Glu Ala Lys Ala Leu Leu Thr His
245 250 255

Ile Gly Ala Glu Thr Ser Leu Arg Tyr Ala Ile His Leu Ile Thr Ala
260 265 270

Ala Ala Leu Ala Cys Gln Lys Arg Lys Gly Lys Leu Val Glu Thr Glu
275 280 285

Asp Ile Ser Arg Ala Tyr Asn Leu Phe Leu Asp Val Lys Arg Ser Thr
290 295 300

Gln Tyr Leu Ile Glu Tyr Gln Asn Gln Tyr Met Phe Asn Glu Ala Pro
305 310 315 320

Val Gly Glu Gly Asp Glu Glu Gly Ala Asn Ala Met Leu Ser
325 330

<210> 9

<211> 420

<212> DNA

<213> *Bruguiera sexangula*

<220>

<221> CDS

<222> (27)..(194)

<400> 9

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Met Gly His Ser Asn Val Trp Asn Ser

1 5

cac ccc aag aac tac ggc cct ggt tcc cgc gcc tgt cgg gtg tgt ggg 101

His Pro Lys Asn Tyr Gly Pro Gly Ser Arg Ala Cys Arg Val Cys Gly

10 15 20 25

aat ccg cac ggg ttg atc agg aag tac gga ctc atg tgc tgc aga cag 149

Asn Pro His Gly Leu Ile Arg Lys Tyr Gly Leu Met Cys Cys Arg Gln

30 35 40

tgc ttc cgt agc aat gcc aag gaa att ggc ttc att aag tac cgc 194

Cys Phe Arg Ser Asn Ala Lys Glu Ile Gly Phe Ile Lys Tyr Arg

45 50 55

tgaatgatat cgatatggcc cagaatggcc tgtggcgggtg cgtgttcgat ttcagtagtt 254

ccccctcttc ggatgagctt taggacaatg ttctcttttag tttatgtatt gttgaacttg 314

gactgatgtt gaactaacga tattctggaa tcatttgata ttctgagagt ttattatttt 374

gatcatcatc ctcttgettc tctgcttaaa aaaaaaaaaa aaaaaa 420

<210> 10

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<212> PRT

<213> *Bruguiera sexangula*

<400> 10

Met Gly His Ser Asn Val Trp Asn Ser His Pro Lys Asn Tyr Gly Pro

1 5 10 15

Gly Ser Arg Ala Cys Arg Val Cys Gly Asn Pro His Gly Leu Ile Arg

20 25 30

Lys Tyr Gly Leu Met Cys Cys Arg Gln Cys Phe Arg Ser Asn Ala Lys

35 40 45

Glu Ile Gly Phe Ile Lys Tyr Arg

50 55

<210> 11

<211> 1664

<212> DNA

<213> *Bruguiera sexangula*

<220>

<221> CDS

<222> (34)..(1380)

<400> 11

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Met Gly Lys Glu Lys Ile His

1 5

att aac att gtg gtt att ggc cat gtc gac tcc gga aag tca acc aca 102

Ile Asn Ile Val Val Ile Gly His Val Asp Ser Gly Lys Ser Thr Thr

10 15 20

act ggc cac ttg att tac aag ctt gga ggt atc gac aag cgt gtg att	150
Thr Gly His Leu Ile Tyr Lys Leu Gly Gly Ile Asp Lys Arg Val Ile	
25 30 35	
gag agg ttt gag aag gaa gct gct gag atg aac aag agg tca ttc aag	198
Glu Arg Phe Glu Lys Glu Ala Ala Glu Met Asn Lys Arg Ser Phe Lys	
40 45 50 55	
tat gcc tgg gtg ctt gac aag ctg aag gct gag cgt gag cgt ggt atc	246
Tyr Ala Trp Val Leu Asp Lys Leu Lys Ala Glu Arg Glu Arg Gly Ile	
60 65 70	
acc att gat att gcc ttg tgg aag ttc gag aca acc aaa tat tac tgc	294
Thr Ile Asp Ile Ala Leu Trp Lys Phe Glu Thr Thr Lys Tyr Tyr Cys	
75 80 85	
acg gtc att gat gct cct gga cat cgt gac ttt att aag aat atg atc	342
Thr Val Ile Asp Ala Pro Gly His Arg Asp Phe Ile Lys Asn Met Ile	
90 95 100	
acc ggg act tcc caa gct gac tgt gct gtc ctc atc att gac tct acc	390
Thr Gly Thr Ser Gln Ala Asp Cys Ala Val Leu Ile Ile Asp Ser Thr	
105 110 115	
act ggt ggc ttt gag gct ggt atc tct aaa gat ggt cag acc cgc gag	438
Thr Gly Gly Phe Glu Ala Gly Ile Ser Lys Asp Gly Gln Thr Arg Glu	
120 125 130 135	
cat gcc ctg ctt gcc ttc acc ctt ggt gtt aag caa atg att tgc tgc	486
His Ala Leu Leu Ala Phe Thr Leu Gly Val Lys Gln Met Ile Cys Cys	
140 145 150	
tgc aac aag atg gat gct acc act tcc aag tat tct aag gca aga tat	534
Cys Asn Lys Met Asp Ala Thr Thr Ser Lys Tyr Ser Lys Ala Arg Tyr	
155 160 165	

gat gaa att gtt aag gaa gtg tca tcc tac ttg aag aag gtt ggt tac	582
Asp Glu Ile Val Lys Glu Val Ser Ser Tyr Leu Lys Lys Val Gly Tyr	
170 175 180	
aac cca gag aag att cct ttt gtc ccc ata tct gga ttt gag ggt gac	630
Asn Pro Glu Lys Ile Pro Phe Val Pro Ile Ser Gly Phe Glu Gly Asp	
185 190 195	
aac atg att gag aga tcc acc aac ctt gac tgg tac aag ggc cca act	678
Asn Met Ile Glu Arg Ser Thr Asn Leu Asp Trp Tyr Lys Gly Pro Thr	
200 205 210 215	
ctt ctt gag gcc ctg gac atg atc cag gag cca aag agg cca tca gat	726
Leu Leu Glu Ala Leu Asp Met Ile Gln Glu Pro Lys Arg Pro Ser Asp	
220 225 230	
aag ccc ctc cgt ctc cca ctt cag gat gtg tac aag att ggt ggt att	774
Lys Pro Leu Arg Leu Pro Leu Gln Asp Val Tyr Lys Ile Gly Gly Ile	
235 240 245	
ggg aca gtc cca gtg ggt cgt gtt gaa act ggt gtc ctg aag cct gga	822
Gly Thr Val Pro Val Gly Arg Val Glu Thr Gly Val Leu Lys Pro Gly	
250 255 260	
atg gtt gtt act ttt ggt ccc tca gga ctg acc act gaa gtt aag tct	870
Met Val Val Thr Phe Gly Pro Ser Gly Leu Thr Thr Glu Val Lys Ser	
265 270 275	
gtg gag atg cac cat gaa gct ctc caa gag gct ctt ccc gga gac aac	918
Val Glu Met His His Glu Ala Leu Gln Glu Ala Leu Pro Gly Asp Asn	
280 285 290 295	
gtt ggc ttc aat gtt aag aat gtt tcc gtg aag gat ctt aag cgg ggt	966
Val Gly Phe Asn Val Lys Asn Val Ser Val Lys Asp Leu Lys Arg Gly	
300 305 310	

tat gtt gcc tca aac tcc aag gat gat cct gcc aag gag gca tct agc	1014
Tyr Val Ala Ser Asn Ser Lys Asp Asp Pro Ala Lys Glu Ala Ser Ser	
315 320 325	
ttc acc tcc caa gtt atc atc atg aac cac cct ggt cag att gga aat	1062
Phe Thr Ser Gln Val Ile Ile Met Asn His Pro Gly Gln Ile Gly Asn	
330 335 340	
ggt tat gcc cct gtt ctg gat tgc cac acc tct cac att gct gtc aag	1110
Gly Tyr Ala Pro Val Leu Asp Cys His Thr Ser His Ile Ala Val Lys	
345 350 355	
ttt tct gag atc ctc aca aag att gat agg cga tct ggc aag gag ctt	1158
Phe Ser Glu Ile Leu Thr Lys Ile Asp Arg Arg Ser Gly Lys Glu Leu	
360 365 370 375	
gaa aag gag ccc aag ttc ttg aag aat ggt gat gct ggg ttc gtg aag	1206
Glu Lys Glu Pro Lys Phe Leu Lys Asn Gly Asp Ala Gly Phe Val Lys	
380 385 390	
atg att ccg acc aag cct atg gtg gtg gaa act ttc tcc gag tat cct	1254
Met Ile Pro Thr Lys Pro Met Val Val Glu Thr Phe Ser Glu Tyr Pro	
395 400 405	
ccg ctt ggt aga ttt gcc gtc agg gac atg cgc cag act gtt gca gtg	1302
Pro Leu Gly Arg Phe Ala Val Arg Asp Met Arg Gln Thr Val Ala Val	
410 415 420	
gga gtc atc aag agt gtc gag aaa aag gaa cct tct gga gct aag gtg	1350
Gly Val Ile Lys Ser Val Glu Lys Lys Glu Pro Ser Gly Ala Lys Val	
425 430 435	
act aaa tct gct gcc aag aag ggt ggc aaa tgaaccgtgc aagtcagagt	1400
Thr Lys Ser Ala Ala Lys Lys Gly Gly Lys	
440 445	

tgatgtagat gaaggtatt ggaagaataa agactgggcc ctggttagcg gtctaattat 1460
 tggatgttca gcagttggtt tcgagaacta cagtttcaat tcagcgccat catcacggag 1520
 ctgttggtcc cagaattggg ttcttgaccg tcggtggcat tggctgttgg tttgagtgac 1580
 ttctttgtgt catgtttaga ctttatcgga ttgctatatt cataaagcgg cttgggaatt 1640
 ttaaaaaaaaa aaaaaaaaaa aaaa 1664

<210> 12

<211> 449

<212> PRT

<213> Bruguiera sexangula

<400> 12

Met Gly Lys Glu Lys Ile His Ile Asn Ile Val Val Ile Gly His Val
 1 5 10 15

Asp Ser Gly Lys Ser Thr Thr Thr Gly His Leu Ile Tyr Lys Leu Gly
 20 25 30

Gly Ile Asp Lys Arg Val Ile Glu Arg Phe Glu Lys Glu Ala Ala Glu
 35 40 45

Met Asn Lys Arg Ser Phe Lys Tyr Ala Trp Val Leu Asp Lys Leu Lys
 50 55 60

Ala Glu Arg Glu Arg Gly Ile Thr Ile Asp Ile Ala Leu Trp Lys Phe
 65 70 75 80

Glu Thr Thr Lys Tyr Tyr Cys Thr Val Ile Asp Ala Pro Gly His Arg
 85 90 95

Asp Phe Ile Lys Asn Met Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala
100 105 110

Val Leu Ile Ile Asp Ser Thr Thr Gly Gly Phe Glu Ala Gly Ile Ser
115 120 125

Lys Asp Gly Gln Thr Arg Glu His Ala Leu Leu Ala Phe Thr Leu Gly
130 135 140

Val Lys Gln Met Ile Cys Cys Cys Asn Lys Met Asp Ala Thr Thr Ser
145 150 155 160

Lys Tyr Ser Lys Ala Arg Tyr Asp Glu Ile Val Lys Glu Val Ser Ser
165 170 175

Tyr Leu Lys Lys Val Gly Tyr Asn Pro Glu Lys Ile Pro Phe Val Pro
180 185 190

Ile Ser Gly Phe Glu Gly Asp Asn Met Ile Glu Arg Ser Thr Asn Leu
195 200 205

Asp Trp Tyr Lys Gly Pro Thr Leu Leu Glu Ala Leu Asp Met Ile Gln
210 215 220

Glu Pro Lys Arg Pro Ser Asp Lys Pro Leu Arg Leu Pro Leu Gln Asp
225 230 235 240

Val Tyr Lys Ile Gly Gly Ile Gly Thr Val Pro Val Gly Arg Val Glu
245 250 255

Thr Gly Val Leu Lys Pro Gly Met Val Val Thr Phe Gly Pro Ser Gly
260 265 270

Leu Thr Thr Glu Val Lys Ser Val Glu Met His His Glu Ala Leu Gln
275 280 285

Glu Ala Leu Pro Gly Asp Asn Val Gly Phe Asn Val Lys Asn Val Ser
290 295 300

Val Lys Asp Leu Lys Arg Gly Tyr Val Ala Ser Asn Ser Lys Asp Asp
305 310 315 320

Pro Ala Lys Glu Ala Ser Ser Phe Thr Ser Gln Val Ile Ile Met Asn
325 330 335

His Pro Gly Gln Ile Gly Asn Gly Tyr Ala Pro Val Leu Asp Cys His
340 345 350

Thr Ser His Ile Ala Val Lys Phe Ser Glu Ile Leu Thr Lys Ile Asp
355 360 365

Arg Arg Ser Gly Lys Glu Leu Glu Lys Glu Pro Lys Phe Leu Lys Asn
370 375 380

Gly Asp Ala Gly Phe Val Lys Met Ile Pro Thr Lys Pro Met Val Val
385 390 395 400

Glu Thr Phe Ser Glu Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp
405 410 415

Met Arg Gln Thr Val Ala Val Gly Val Ile Lys Ser Val Glu Lys Lys
420 425 430

Glu Pro Ser Gly Ala Lys Val Thr Lys Ser Ala Ala Lys Lys Gly Gly
435 440 445

Lys

<211> 770

<212> DNA

<213> *Bruguiera sexangula*

<220>

<221> CDS

<222> (2).. (769)

<400> 13

c gat gat atg gac gag gcc aca ccc acc ttt gtt tgg ggc acc aat atc 49

Asp Asp Met Asp Glu Ala Thr Pro Thr Phe Val Trp Gly Thr Asn Ile

1 5 10 15

agc gtg cag gat gtc aag gcc gct att cag atg ttt ttg aag cac ttc 97

Ser Val Gln Asp Val Lys Ala Ala Ile Gln Met Phe Leu Lys His Phe

20 25 30

agg gat agt aat cag agt caa agg aac gag att ttt gaa gaa ggg aag 145

Arg Asp Ser Asn Gln Ser Gln Arg Asn Glu Ile Phe Glu Glu Gly Lys

35 40 45

tac gtg aaa gcg ata cat aag gtt ctt gaa gtt gaa gga gag tcg ctt 193

Tyr Val Lys Ala Ile His Lys Val Leu Glu Val Glu Gly Glu Ser Leu

50 55 60

gat gtt gat gct cgt gat gtg ttt gat tat gat tct gat ttg tat gcc 241

Asp Val Asp Ala Arg Asp Val Phe Asp Tyr Asp Ser Asp Leu Tyr Ala

65 70 75 80

aag atg att cgg tac cca ctt gag gtt ttg gcc att ttc gac att gtt 289

Lys Met Ile Arg Tyr Pro Leu Glu Val Leu Ala Ile Phe Asp Ile Val

85 90 95

ttg atg gat att gtg agt ttg atc aac cct ttg ttt gag aaa cat gta 337

Leu Met Asp Ile Val Ser Leu Ile Asn Pro Leu Phe Glu Lys His Val

100 105 110

caa gtc agg att ttc aat ctt aag acc tcg att aca atg aga aat ctc	385
Gln Val Arg Ile Phe Asn Leu Lys Thr Ser Ile Thr Met Arg Asn Leu	
115 120 125	
aac cct tct gat atc gaa aag atg gtg tca ttg aag gga atg ata att	433
Asn Pro Ser Asp Ile Glu Lys Met Val Ser Leu Lys Gly Met Ile Ile	
130 135 140	
cgg tgt agt tcc ata ata ccg gag atc agg gaa gca gta ttt aga tgc	481
Arg Cys Ser Ser Ile Ile Pro Glu Ile Arg Glu Ala Val Phe Arg Cys	
145 150 155 160	
ctt gtt tgt ggc tac ttc tct gat ccc atc gtt gtg gat aga gga cgg	529
Leu Val Cys Gly Tyr Phe Ser Asp Pro Ile Val Val Asp Arg Gly Arg	
165 170 175	
ata agt gaa cct aaa gca tgc ttg aaa gag gaa tgt ctt act aag aac	577
Ile Ser Glu Pro Lys Ala Cys Leu Lys Glu Glu Cys Leu Thr Lys Asn	
180 185 190	
tcc atg aca cta gtt cac aat cgt tgc agg ttt gct gat aag cag att	625
Ser Met Thr Leu Val His Asn Arg Cys Arg Phe Ala Asp Lys Gln Ile	
195 200 205	
gtg agg ctc cag gag aca cct gac gag atc cct gaa gga gga aca cca	673
Val Arg Leu Gln Glu Thr Pro Asp Glu Ile Pro Glu Gly Gly Thr Pro	
210 215 220	
cac acg gtg agc tta ttg atg cat gac aag ctg gta gat gct gga aag	721
His Thr Val Ser Leu Leu Met His Asp Lys Leu Val Asp Ala Gly Lys	
225 230 235 240	
cca ggt gac agg gtt gag gtc act gga att tat agg gct atg agt gtt a	770
Pro Gly Asp Arg Val Glu Val Thr Gly Ile Tyr Arg Ala Met Ser Val	
245 250 255	

<210> 14

<211> 256

<212> PRT

<213> Bruguiera sexangula

<400> 14

Asp Asp Met Asp Glu Ala Thr Pro Thr Phe Val Trp Gly Thr Asn Ile
1 5 10 15

Ser Val Gln Asp Val Lys Ala Ala Ile Gln Met Phe Leu Lys His Phe
20 25 30

Arg Asp Ser Asn Gln Ser Gln Arg Asn Glu Ile Phe Glu Glu Gly Lys
35 40 45

Tyr Val Lys Ala Ile His Lys Val Leu Glu Val Glu Gly Glu Ser Leu
50 55 60

Asp Val Asp Ala Arg Asp Val Phe Asp Tyr Asp Ser Asp Leu Tyr Ala
65 70 75 80

Lys Met Ile Arg Tyr Pro Leu Glu Val Leu Ala Ile Phe Asp Ile Val
85 90 95

Leu Met Asp Ile Val Ser Leu Ile Asn Pro Leu Phe Glu Lys His Val
100 105 110

Gln Val Arg Ile Phe Asn Leu Lys Thr Ser Ile Thr Met Arg Asn Leu
115 120 125

Asn Pro Ser Asp Ile Glu Lys Met Val Ser Leu Lys Gly Met Ile Ile
130 135 140

Arg Cys Ser Ser Ile Ile Pro Glu Ile Arg Glu Ala Val Phe Arg Cys

145	150	155	160
Leu Val Cys Gly Tyr Phe Ser Asp Pro Ile Val Val Asp Arg Gly Arg			
165	170	175	
Ile Ser Glu Pro Lys Ala Cys Leu Lys Glu Glu Cys Leu Thr Lys Asn			
180	185	190	
Ser Met Thr Leu Val His Asn Arg Cys Arg Phe Ala Asp Lys Gln Ile			
195	200	205	
Val Arg Leu Gln Glu Thr Pro Asp Glu Ile Pro Glu Gly Gly Thr Pro			
210	215	220	
His Thr Val Ser Leu Leu Met His Asp Lys Leu Val Asp Ala Gly Lys			
225	230	235	240
Pro Gly Asp Arg Val Glu Val Thr Gly Ile Tyr Arg Ala Met Ser Val			
245	250	255	

<210> 15

<211> 846

<212> DNA

<213> Mesembryanthemum crystallinum

<220>

<221> CDS

<222> (39).. (530)

<400> 15

caaattttct ttgctgaate gaatctacaa aatacctg atg ggt cag gtt ctt gac 56

Met Gly Gln Val Leu Asp

aaa ttt caa cgt aag caa tgg aga caa aag caa atc cag aag ata aca	104
Lys Phe Gln Arg Lys Gln Trp Arg Gln Lys Gln Ile Gln Lys Ile Thr	
10 15 20	
gat aag gta ttt gat cgt gtc aaa agt ccg acc gga aat ggc act ctt	152
Asp Lys Val Phe Asp Arg Val Lys Ser Pro Thr Gly Asn Gly Thr Leu	
25 30 35	
aca ttt gaa gag ctg tat ata gct acc ctg att gtc tac aat gat ata	200
Thr Phe Glu Glu Leu Tyr Ile Ala Thr Leu Ile Val Tyr Asn Asp Ile	
40 45 50	
aac aag tat ttg ccg ggg ccg cac ttt gat cct cca tcg aaa gac aaa	248
Asn Lys Tyr Leu Pro Gly Pro His Phe Asp Pro Pro Ser Lys Asp Lys	
55 60 65 70	
atc aga gcc ttg atg cag gaa tgc gat atg gat gtc gat gga gaa ctt	296
Ile Arg Ala Leu Met Gln Glu Cys Asp Met Asp Val Asp Gly Glu Leu	
75 80 85	
aac cgt gag gaa ttt gtg aag ttc atg cag aag gtg aca gcc gat aca	344
Asn Arg Glu Glu Phe Val Lys Phe Met Gln Lys Val Thr Ala Asp Thr	
90 95 100	
ttc tct acg gtc agc cag gga ctg att atc tct ctg att ctg gcg cca	392
Phe Ser Thr Val Ser Gln Gly Leu Ile Ile Ser Leu Ile Leu Ala Pro	
105 110 115	
aca gtt gca ttg gcg acg aag agg gca aca gaa ggt gtt cca ggt gtg	440
Thr Val Ala Leu Ala Thr Lys Arg Ala Thr Glu Gly Val Pro Gly Val	
120 125 130	
ggg aaa gtg gtg caa aag gtg cct act tca att tat gca tcc ctg gtg	488
Gly Lys Val Val Gln Lys Val Pro Thr Ser Ile Tyr Ala Ser Leu Val	
135 140 145 150	

acc ctt gtt gtc gtt gca atc caa act gct agc gag gga tgc 530
 Thr Leu Val Val Val Ala Ile Gln Thr Ala Ser Glu Gly Cys

155 160

tgattagagg ctttagttac ttgttcatga tacagaagga acagtcttgg tcaatttatt 590

tcttttttaa taggacataa ggaagttgta tatctttctt ctttcttcta ccaggttttg 650

ggggaagttg gaaagaacat acaaatgatt tcaactgcgt attggctgat cctcccatTT 710

attaaaactt gtcgtgtcta gcatgagcga ttcaatatTT gcaatatgca atatttgtaa 770

tgatgtctac attcagtgat tagtgtgatt gtgcagtttg ttgggaaaaa aaaaaaaaaa 830

aaaaaaaaaa aaaaaa 846

<210> 16

<211> 164

<212> PRT

<213> Mesembryanthemum crystallinum

<400> 16

Met Gly Gln Val Leu Asp Lys Phe Gln Arg Lys Gln Trp Arg Gln Lys
 1 5 10 15

Gln Ile Gln Lys Ile Thr Asp Lys Val Phe Asp Arg Val Lys Ser Pro
 20 25 30

Thr Gly Asn Gly Thr Leu Thr Phe Glu Glu Leu Tyr Ile Ala Thr Leu
 35 40 45

Ile Val Tyr Asn Asp Ile Asn Lys Tyr Leu Pro Gly Pro His Phe Asp
 50 55 60

Pro Pro Ser Lys Asp Lys Ile Arg Ala Leu Met Gln Glu Cys Asp Met

65		70		75		80
Asp Val Asp Gly Glu Leu Asn Arg Glu Glu Phe Val Lys Phe Met Gln						
	85		90		95	
Lys Val Thr Ala Asp Thr Phe Ser Thr Val Ser Gln Gly Leu Ile Ile						
	100		105		110	
Ser Leu Ile Leu Ala Pro Thr Val Ala Leu Ala Thr Lys Arg Ala Thr						
	115		120		125	
Glu Gly Val Pro Gly Val Gly Lys Val Val Gln Lys Val Pro Thr Ser						
	130		135		140	
Ile Tyr Ala Ser Leu Val Thr Leu Val Val Val Ala Ile Gln Thr Ala						
145		150		155		160
Ser Glu Gly Cys						

<210> 17
 <211> 872
 <212> DNA
 <213> Mesembryanthemum crystallinum

<220>
 <221> CDS
 <222> (183).. (569)

<400> 17
 aacaaaatgt ctctctcttt ctctttctct ttctctttct ctctcttctg gggttgattg 60
 agtaagctct gtccttttgc tctctgttga atgtactatc ttctgtgaac caaaggccaa 120

agattaacta ttggagattt ctctactcga aatttgtttt taggtgttga ccctgttgag 180

ct atg gcg aac aag ccc caa att cca acg aag aat tcg gcc ctc att 227

Met Ala Asn Lys Pro Gln Ile Pro Thr Lys Asn Ser Ala Leu Ile

1

5

10

15

gct att atc gcg gat gag gat act gta act gga ttt ttg ctg gct gga 275

Ala Ile Ile Ala Asp Glu Asp Thr Val Thr Gly Phe Leu Leu Ala Gly

20

25

30

ggt ggt aat gtt gat cta cga aga cag aca aat tac att att gtg gac 323

Val Gly Asn Val Asp Leu Arg Arg Gln Thr Asn Tyr Ile Ile Val Asp

35

40

45

aat aaa aca acg atg aag caa atc gaa gat gca ttc aag gag ttc aca 371

Asn Lys Thr Thr Met Lys Gln Ile Glu Asp Ala Phe Lys Glu Phe Thr

50

55

60

gca aga gag gac att gcg gtt gta cta atc agc caa tat gtt gca aat 419

Ala Arg Glu Asp Ile Ala Val Val Leu Ile Ser Gln Tyr Val Ala Asn

65

70

75

atg ata aga gta ttg gtt gat agc tac aac aaa cca atc ccg gca att 467

Met Ile Arg Val Leu Val Asp Ser Tyr Asn Lys Pro Ile Pro Ala Ile

80

85

90

95

ttg gag att cct tca aag gac cat cct tat gat cct aac cat gat tca 515

Leu Glu Ile Pro Ser Lys Asp His Pro Tyr Asp Pro Asn His Asp Ser

100

105

110

gtc ctt tca agg gtt aaa tac ctg ttc tct tct gaa tcg gca tca agc 563

Val Leu Ser Arg Val Lys Tyr Leu Phe Ser Ser Glu Ser Ala Ser Ser

115

120

125

aga ttt tagccatgatg ctttgtaaag ttccctgctc ctgaatgttt ggtgattatg 619

Arg Phe

agtttaaact agaaccagtc acattctgac ttggtathtt gaggcactgt ttgttttatg 679

ttcttaaaat aaggagtgtta attacgactc catgaatcgg gatatgactc catgaatcgc 739

atgtatttct ttccatctca ttgaaagag tcgagcagcc atatcattta gtttcttcct 799

cttgcgatg agcttggaag aaatgttttg gctataaaag atttcaactc ttgtacaaa 859

aaaaaaaaa aaa 872

<210> 18

<211> 129

<212> PRT

<213> Mesembryanthemum crystallinum

<400> 18

Met Ala Asn Lys Pro Gln Ile Pro Thr Lys Asn Ser Ala Leu Ile Ala
1 5 10 15

Ile Ile Ala Asp Glu Asp Thr Val Thr Gly Phe Leu Leu Ala Gly Val
20 25 30

Gly Asn Val Asp Leu Arg Arg Gln Thr Asn Tyr Ile Ile Val Asp Asn
35 40 45

Lys Thr Thr Met Lys Gln Ile Glu Asp Ala Phe Lys Glu Phe Thr Ala
50 55 60

Arg Glu Asp Ile Ala Val Val Leu Ile Ser Gln Tyr Val Ala Asn Met
65 70 75 80

Ile Arg Val Leu Val Asp Ser Tyr Asn Lys Pro Ile Pro Ala Ile Leu
85 90 95

Glu Ile Pro Ser Lys Asp His Pro Tyr Asp Pro Asn His Asp Ser Val
100 105 110

Leu Ser Arg Val Lys Tyr Leu Phe Ser Ser Glu Ser Ala Ser Ser Arg
115 120 125

Phe

<210> 19

<211> 647

<212> DNA

<213> Mesembryanthemum crystallinum

<220>

<221> CDS

<222> (64)..(426)

<400> 19

cttgtttttc tctctcctct ctctctctct tctccgcacc ctcaggcagt gaaggtagca 60

aca atg gcg tac gcg atg aag cca acg aag ccc ggg atg gag gaa tcc 108
Met Ala Tyr Ala Met Lys Pro Thr Lys Pro Gly Met Glu Glu Ser
1 5 10 15

cag gag cag att cac aag atc agg atc act ctt tct tct aag aac gtc 156
Gln Glu Gln Ile His Lys Ile Arg Ile Thr Leu Ser Ser Lys Asn Val
20 25 30

aag aac ctt gag aaa gtg tgt gct gat ctt gta cgc ggt gca aag gac 204
Lys Asn Leu Glu Lys Val Cys Ala Asp Leu Val Arg Gly Ala Lys Asp
35 40 45

aag cgc ctc agg gtt aag gga cca gtg agg atg ccc acc aag gtt ctg 252

Lys Arg Leu Arg Val Lys Gly Pro Val Arg Met Pro Thr Lys Val Leu
50 55 60

aag atc aca aca agg aag tct ccc tgt ggt gaa gga acc aac acc ttt 300
Lys Ile Thr Thr Arg Lys Ser Pro Cys Gly Glu Gly Thr Asn Thr Phe
65 70 75

gac aga ttt gag ttg cgt gtt cac aag aga gtc att gac ctc ttc agc 348
Asp Arg Phe Glu Leu Arg Val His Lys Arg Val Ile Asp Leu Phe Ser
80 85 90 95

tcc cca gac gtg gtc aag cag atc acc tcc atc acc att gaa cct ggt 396
Ser Pro Asp Val Val Lys Gln Ile Thr Ser Ile Thr Ile Glu Pro Gly
100 105 110

gtt gag gtt gag gtt aca ata gct gac tct tagacatgcc tgttgaagtt 446
Val Glu Val Glu Val Thr Ile Ala Asp Ser
115 120

gtcgtcgttg tagggctgtt gtagctgtct catatagtgg tgctatctca ctaagaattt 506

tgaagatact aaattgtttg ttgaaagag atgttttctt tagctgtaat gttatgtttt 566

tgaagggtgtt ggaacatgca ttatttgta atgctttatc aatagaactt ccaatttgaa 626

tgcaaaaaaa aaaaaaaaaa a 647

<210> 20

<211> 121

<212> PRT

<213> Mesembryanthemum crystallinum

<400> 20

Met Ala Tyr Ala Met Lys Pro Thr Lys Pro Gly Met Glu Glu Ser Gln
1 5 10 15

Glu Gln Ile His Lys Ile Arg Ile Thr Leu Ser Ser Lys Asn Val Lys
 20 25 30
 Asn Leu Glu Lys Val Cys Ala Asp Leu Val Arg Gly Ala Lys Asp Lys
 35 40 45
 Arg Leu Arg Val Lys Gly Pro Val Arg Met Pro Thr Lys Val Leu Lys
 50 55 60
 Ile Thr Thr Arg Lys Ser Pro Cys Gly Glu Gly Thr Asn Thr Phe Asp
 65 70 75 80
 Arg Phe Glu Leu Arg Val His Lys Arg Val Ile Asp Leu Phe Ser Ser
 85 90 95
 Pro Asp Val Val Lys Gln Ile Thr Ser Ile Thr Ile Glu Pro Gly Val
 100 105 110
 Glu Val Glu Val Thr Ile Ala Asp Ser
 115 120

<210> 21

<211> 686

<212> DNA

<213> Sueada japonica

<220>

<221> CDS

<222> (62).. (493)

<400> 21

acaccattca caaaacacat taaaaaaaaa cactacttct ttctttctta gccacttgaa 60

a atg gcc tac tca aag gct gta ctc ctt gcc ctt atc ttt gct gtg act 109

Met Ala Tyr Ser Lys Ala Val Leu Leu Ala Leu Ile Phe Ala Val Thr

1 5 10 15

ctt gtc att gcc tct cag gtc tca gct cgt gaa ctt gct gag gag aca 157

Leu Val Ile Ala Ser Gln Val Ser Ala Arg Glu Leu Ala Glu Glu Thr

20 25 30

caa tct gtg gag gag tct aag gga tac ggt ggt ggg cac gga ggt cac 205

Gln Ser Val Glu Glu Ser Lys Gly Tyr Gly Gly Gly His Gly Gly His

35 40 45

tat ggt ggt ggt cac tat ggt ggt gga cac aga cac ggt ggc cat gga 253

Tyr Gly Gly Gly His Tyr Gly Gly Gly His Arg His Gly Gly His Gly

50 55 60

cac tac gca act gag gaa gca gag aac aag aat gaa gcc gta gaa cct 301

His Tyr Ala Thr Glu Glu Ala Glu Asn Lys Asn Glu Ala Val Glu Pro

65 70 75 80

caa ggc ggc tat ggt cac gga cac gga gga ggc tac gga cac ggt ggt 349

Gln Gly Gly Tyr Gly His Gly His Gly Gly Gly Tyr Gly His Gly Gly

85 90 95

ggc tac gga cac ggt gga ggc tac gga cac gga ggt ggc tac ggg cac 397

Gly Tyr Gly His Gly Gly Gly Tyr Gly His Gly Gly Gly Tyr Gly His

100 105 110

ggt ggt ggc tac gga cat gga ggt ggt tat gga cac ggt gga cac ggt 445

Gly Gly Gly Tyr Gly His Gly Gly Gly Tyr Gly His Gly Gly His Gly

115 120 125

gga cat ggt ggt cat ggt cac tac gcc aag act acc gag gaa caa aat 493

Gly His Gly Gly His Gly His Tyr Ala Lys Thr Thr Glu Glu Gln Asn

130 135 140

taagttatgg gttactaaaa cttaaattgt acgttgtaa ataaaatgta ctttatgatt 553

ttacatgagt atgcatgtaa ttcatacataa gcttcaagga ctatcttgta ctctatgtta 613

tataacctata tgaaatggaa gcgtgacttt tattactgta aaaaaaaaaa aaaaaaaaaa 673

aaaaaaaaaa aaa 686

<210> 22

<211> 144

<212> PRT

<213> Sueada japonica

<400> 22

Met Ala Tyr Ser Lys Ala Val Leu Leu Ala Leu Ile Phe Ala Val Thr

1 5 10 15

Leu Val Ile Ala Ser Gln Val Ser Ala Arg Glu Leu Ala Glu Glu Thr

20 25 30

Gln Ser Val Glu Glu Ser Lys Gly Tyr Gly Gly Gly His Gly Gly His

35 40 45

Tyr Gly Gly Gly His Tyr Gly Gly Gly His Arg His Gly Gly His Gly

50 55 60

His Tyr Ala Thr Glu Glu Ala Glu Asn Lys Asn Glu Ala Val Glu Pro

65 70 75 80

Gln Gly Gly Tyr Gly His Gly His Gly Gly Gly Tyr Gly His Gly Gly

85 90 95

Gly Tyr Gly His Gly Gly Gly Tyr Gly His Gly Gly Gly Tyr Gly His

100 105 110

Gly Gly Gly Tyr Gly His Gly Gly Gly Tyr Gly His Gly Gly His Gly
115 120 125

Gly His Gly Gly His Gly His Tyr Ala Lys Thr Thr Glu Glu Gln Asn
130 135 140

<210> 23

<211> 683

<212> DNA

<213> Salsola komarovii

<220>

<221> CDS

<222> (48).. (362)

<400> 23

gttaagatat tatattgcaa ctttacaaag catttctgca actaaat atg gcc ttt 56
Met Ala Phe
1

tcc aaa cct cta att gct tct cta ctt ctt tct ctc ttt gtt ctt cag 104
Ser Lys Pro Leu Ile Ala Ser Leu Leu Leu Ser Leu Phe Val Leu Gln
5 10 15

ttt gtt cat gca gtt gaa cct att tca tcc tcc aat caa gtg ggt agc 152
Phe Val His Ala Val Glu Pro Ile Ser Ser Ser Asn Gln Val Gly Ser
20 25 30 35

aac act gga ggt acc tca gag agt aaa gtg gat tgt ggg gcg gca tgt 200
Asn Thr Gly Gly Thr Ser Glu Ser Lys Val Asp Cys Gly Ala Ala Cys
40 45 50

acg gtg agg tgc agc gcc tcg aag agg cca aac cta tgc aac agg tca 248
Thr Val Arg Cys Ser Ala Ser Lys Arg Pro Asn Leu Cys Asn Arg Ser

55	60	65	
tgt ggc agt tgt tgc aag acg tgc aac tgc gtg cca cca ggc act tcc	296		
Cys Gly Ser Cys Cys Lys Thr Cys Asn Cys Val Pro Pro Gly Thr Ser			
70	75	80	
ggc aac tac gaa gcc tgc cct tgt tac gcc aac ttg acc acc cac ggc	344		
Gly Asn Tyr Glu Ala Cys Pro Cys Tyr Ala Asn Leu Thr Thr His Gly			
85	90	95	
aat cga cac aag tgc cct taattaacaa gaattgttta gttgtttatt	392		
Asn Arg His Lys Cys Pro			
100	105		
acatccgtac catgtaacgt actcctatatt acactactag agtactagta ataaacattt	452		
ttaggcacgg tccagttgtt catgtagcta gtggtatatt gagtcataaa tgagtgattg	512		
aaaatgagat atgataaaag tgtattatct acattgtagt actgttttgt atcatagtgt	572		
agtgatgttt atttttcgta cctttaattt gttactttgt attccctttc attctatcta	632		
tttacaatcc ttttgaagt ttatgtgaaa aaaaaaaaaa aaaaaaaaaa a	683		

<210> 24

<211> 105

<212> PRT

<213> Salsola komarovii

<400> 24

Met	Ala	Phe	Ser	Lys	Pro	Leu	Ile	Ala	Ser	Leu	Leu	Leu	Ser	Leu	Phe
1				5				10					15		

Val	Leu	Gln	Phe	Val	His	Ala	Val	Glu	Pro	Ile	Ser	Ser	Ser	Asn	Gln
		20					25						30		

Val Gly Ser Asn Thr Gly Gly Thr Ser Glu Ser Lys Val Asp Cys Gly
 35 40 45

Ala Ala Cys Thr Val Arg Cys Ser Ala Ser Lys Arg Pro Asn Leu Cys
 50 55 60

Asn Arg Ser Cys Gly Ser Cys Cys Lys Thr Cys Asn Cys Val Pro Pro
 65 70 75 80

Gly Thr Ser Gly Asn Tyr Glu Ala Cys Pro Cys Tyr Ala Asn Leu Thr
 85 90 95

Thr His Gly Asn Arg His Lys Cys Pro
 100 105

<210> 25

<211> 803

<212> DNA

<213> Salsola komarovii

<220>

<221> CDS

<222> (51).. (593)

<400> 25

cgcagacgct tcagctcttt ctctctcttt ctctctcttc accgtgaaag atg ggg 56

Met Gly

1

ttg tca ttt acc aaa ttg ttt agc cgg ttg ttc gct aag aag gaa atg 104

Leu Ser Phe Thr Lys Leu Phe Ser Arg Leu Phe Ala Lys Lys Glu Met

5

10

15

cgt atc ctt atg gtc ggt ctc gat gcc gct ggt aaa acc acc att ctc	152
Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr Ile Leu	
20 25 30	

tat aaa ctc aag ctg gga gag att gtc acc acc att cct acc att gga	200
Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr Ile Gly	
35 40 45 50	

ttt aat gtg gag act gta gaa tac aag aac atc agc ttc act gtg tgg	248
Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Ser Phe Thr Val Trp	
55 60 65	

gat gtc ggg ggt caa gac aag att cgt cca ttg tgg aga cat tac ttc	296
Asp Val Gly Gly Gln Asp Lys Ile Arg Pro Leu Trp Arg His Tyr Phe	
70 75 80	

caa aac acc caa ggt ctc atc ttt gtg gtt gac agt aat gat cgt gac	344
Gln Asn Thr Gln Gly Leu Ile Phe Val Val Asp Ser Asn Asp Arg Asp	
85 90 95	

cgt gtc gtt gag gca aga gat gaa ctg cat agg atg tta aat gag gat	392
Arg Val Val Glu Ala Arg Asp Glu Leu His Arg Met Leu Asn Glu Asp	
100 105 110	

gaa tta cga gat gca gtg ttg ttg gtg ttt gca aac aag caa gat ctt	440
Glu Leu Arg Asp Ala Val Leu Leu Val Phe Ala Asn Lys Gln Asp Leu	
115 120 125 130	

ccc aat gca atg aat gct gct gag atc act gat aag ctt ggt ctc cat	488
Pro Asn Ala Met Asn Ala Ala Glu Ile Thr Asp Lys Leu Gly Leu His	
135 140 145	

tct cta cgt caa cgc cat tgg tac ata caa agc aca tgt gcc acc tet	536
Ser Leu Arg Gln Arg His Trp Tyr Ile Gln Ser Thr Cys Ala Thr Ser	
150 155 160	

gga gaa ggg ctt tac gag ggt ctg gac tgg ctc tca aac aat atc gct 584
 Gly Glu Gly Leu Tyr Glu Gly Leu Asp Trp Leu Ser Asn Asn Ile Ala
 165 170 175

agc aag gct taaaagtaac agaacgagta aggttagctt tctcagagaa 633
 Ser Lys Ala
 180

gaagctggag tataggctga ggactatcgt tactgctagt gttacccttt ttatttttgc 693

catttatatg ttcacatfff tggttcctat cggacaagaa ttattttctg cgtttatgtt 753

gacttggttat aataccatac ttttttagttg aaaaaaaaaa aaaaaaaaaa 803

<210> 26

<211> 181

<212> PRT

<213> Salsola komarovii

<400> 26

Met Gly Leu Ser Phe Thr Lys Leu Phe Ser Arg Leu Phe Ala Lys Lys
 1 5 10 15

Glu Met Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr
 20 25 30

Ile Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr
 35 40 45

Ile Gly Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Ser Phe Thr
 50 55 60

Val Trp Asp Val Gly Gly Gln Asp Lys Ile Arg Pro Leu Trp Arg His
 65 70 75 80

Tyr Phe Gln Asn Thr Gln Gly Leu Ile Phe Val Val Asp Ser Asn Asp
85 90 95

Arg Asp Arg Val Val Glu Ala Arg Asp Glu Leu His Arg Met Leu Asn
100 105 110

Glu Asp Glu Leu Arg Asp Ala Val Leu Leu Val Phe Ala Asn Lys Gln
115 120 125

Asp Leu Pro Asn Ala Met Asn Ala Ala Glu Ile Thr Asp Lys Leu Gly
130 135 140

Leu His Ser Leu Arg Gln Arg His Trp Tyr Ile Gln Ser Thr Cys Ala
145 150 155 160

Thr Ser Gly Glu Gly Leu Tyr Glu Gly Leu Asp Trp Leu Ser Asn Asn
165 170 175

Ile Ala Ser Lys Ala
180

<210> 27

<211> 680

<212> DNA

<213> Avicennia marina

<220>

<221> CDS

<222> (161).. (454)

<400> 27

ctaaaagcca aaggcaagat aagaaacagg ttccttttagc tatcttcctc gtctcgtgc 60

tgcaaaagtt ccatccccag aagatcagga aaacccttct gcagcagcac tctaataatc 120

ctccaatttt gattcaagag aagaaacaaa ataacagaa atg gct cgc tct ttc 175

Met Ala Arg Ser Phe

1 5

tcc aac gct aag acc gtc tct gct gtc att gcc aac gaa atc tca gct 223

Ser Asn Ala Lys Thr Val Ser Ala Val Ile Ala Asn Glu Ile Ser Ala

10 15 20

ctt gtc acc agg agg ggt tat gct gct ctc gca cag ggc gtt gtt tcg 271

Leu Val Thr Arg Arg Gly Tyr Ala Ala Leu Ala Gln Gly Val Val Ser

25 30 35

agc agc gcg aga agc ggc ggc gct ccg aac gtg atg ctg aag aaa gga 319

Ser Ser Ala Arg Ser Gly Gly Ala Pro Asn Val Met Leu Lys Lys Gly

40 45 50

tcc gaa gaa tcc ggg aag aca gca tgg gtg ccc gac ccg gac acc ggc 367

Ser Glu Glu Ser Gly Lys Thr Ala Trp Val Pro Asp Pro Asp Thr Gly

55 60 65

tac tac cga ccg gga aac gag gac aag gcc gcg ctg gac ccg gtc gag 415

Tyr Tyr Arg Pro Gly Asn Glu Asp Lys Ala Ala Leu Asp Pro Val Glu

70 75 80 85

ctg cgg gag atg ctc atc aag aac aag ccc agc cga caa tgaatgaacc 464

Leu Arg Glu Met Leu Ile Lys Asn Lys Pro Ser Arg Gln

90 95

aagaattgtg ggattctcat taattcctcc cctgttctgg tccatcgtcg gaatctgaac 524

ctgttggtcg tctagaaatt cgttcccatg gaaatctatc aaagtctgta ttcttgccat 584

ggctcttcct gtcccatata tgtatgtcct caggtgtggc ctgggggtggt ttgatagata 644

tataaaatgt ggtgaattta aaaaaaaaaa aaaaaa 680

<210> 28

<211> 98

<212> PRT

<213> Avicennia marina

<400> 28

Met Ala Arg Ser Phe Ser Asn Ala Lys Thr Val Ser Ala Val Ile Ala
1 5 10 15

Asn Glu Ile Ser Ala Leu Val Thr Arg Arg Gly Tyr Ala Ala Leu Ala
20 25 30

Gln Gly Val Val Ser Ser Ser Ala Arg Ser Gly Gly Ala Pro Asn Val
35 40 45

Met Leu Lys Lys Gly Ser Glu Glu Ser Gly Lys Thr Ala Trp Val Pro
50 55 60

Asp Pro Asp Thr Gly Tyr Tyr Arg Pro Gly Asn Glu Asp Lys Ala Ala
65 70 75 80

Leu Asp Pro Val Glu Leu Arg Glu Met Leu Ile Lys Asn Lys Pro Ser
85 90 95

Arg Gln

<210> 29

<211> 490

<212> DNA

<213> Avicennia marina

<220>

<221> CDS

<222> (20).. (349)

<400> 29

tcggctgggc aaagaaggg atg gcg att cca tcg gaa att cgg gac ttt att 52

Met Ala Ile Pro Ser Glu Ile Arg Asp Phe Ile

1 5 10

gct agc cgc aac aga tct ttg gtg atc gca tct cca aag gaa gat gag 100

Ala Ser Arg Asn Arg Ser Leu Val Ile Ala Ser Pro Lys Glu Asp Glu

15 20 25

aaa att ctc cgc tca agg cag tgc acc gaa gaa ggg gcg cgt gca gga 148

Lys Ile Leu Arg Ser Arg Gln Cys Thr Glu Glu Gly Ala Arg Ala Gly

30 35 40

gcc aaa gct gct gca gtt gct tgc gtt gcc agc gcc att ccc act ctg 196

Ala Lys Ala Ala Ala Val Ala Cys Val Ala Ser Ala Ile Pro Thr Leu

45 50 55

gta gct gtt cga acg att ccg tgg gca aag gca aac ctc aac tat aca 244

Val Ala Val Arg Thr Ile Pro Trp Ala Lys Ala Asn Leu Asn Tyr Thr

60 65 70 75

gcc cag gca ctc att ata tct tct gca tcc ata gcg gca tac ttt atc 292

Ala Gln Ala Leu Ile Ile Ser Ser Ala Ser Ile Ala Ala Tyr Phe Ile

80 85 90

gct gct gac aaa acc atc tta gag tgc gca cgg aaa aat gca gag tac 340

Ala Ala Asp Lys Thr Ile Leu Glu Cys Ala Arg Lys Asn Ala Glu Tyr

95 100 105

aaa tcg gct taagatgatg tgtaagacaa tgtgctcagc ttgcaatgct 389

Lys Ser Ala

110

tgccatgact tgtgtttatg tgtatttcaa gtttctgaaa ctagcatttt gattttgtgt 449

tccaatgcaa tgagcattat ggaaaaaaaa aaaaaaaaaa a 490

<210> 30

<211> 110

<212> PRT

<213> Avicennia marina

<400> 30

Met Ala Ile Pro Ser Glu Ile Arg Asp Phe Ile Ala Ser Arg Asn Arg

1 5 10 15

Ser Leu Val Ile Ala Ser Pro Lys Glu Asp Glu Lys Ile Leu Arg Ser

20 25 30

Arg Gln Cys Thr Glu Glu Gly Ala Arg Ala Gly Ala Lys Ala Ala Ala

35 40 45

Val Ala Cys Val Ala Ser Ala Ile Pro Thr Leu Val Ala Val Arg Thr

50 55 60

Ile Pro Trp Ala Lys Ala Asn Leu Asn Tyr Thr Ala Gln Ala Leu Ile

65 70 75 80

Ile Ser Ser Ala Ser Ile Ala Ala Tyr Phe Ile Ala Ala Asp Lys Thr

85 90 95

Ile Leu Glu Cys Ala Arg Lys Asn Ala Glu Tyr Lys Ser Ala

100 105 110

<210> 31

<211> 592

<212> DNA

<213> *Avicennia marina*

<220>

<221> CDS

<222> (75).. (320)

<400> 31

gcagtctcag ccttcctgct ctcctgggtgc cttcaaattt gtgaatttct cgagtgctaa 60

aagattcagc caag atg cag aac gaa gag ggg caa aac atg gat ctc tac 110

Met Gln Asn Glu Glu Gly Gln Asn Met Asp Leu Tyr

1

5

10

atc ccc agg aaa tgc tct gcc acg aac agg ctg atc acc tcc aag gat 158

Ile Pro Arg Lys Cys Ser Ala Thr Asn Arg Leu Ile Thr Ser Lys Asp

15

20

25

cat gct tct gtc cag atc aat gtt ggg cac ttg gat gag aat ggc cga 206

His Ala Ser Val Gln Ile Asn Val Gly His Leu Asp Glu Asn Gly Arg

30

35

40

tac act ggc caa tac tct acc ttt gct ctt tgt gga ttc atc cgt gct 254

Tyr Thr Gly Gln Tyr Ser Thr Phe Ala Leu Cys Gly Phe Ile Arg Ala

45

50

55

60

cag ggt gat gct gac agt gct ctt gat agg ctc tgg cag aaa aag aaa 302

Gln Gly Asp Ala Asp Ser Ala Leu Asp Arg Leu Trp Gln Lys Lys Lys

65

70

75

gtc gaa acc agg cag cag tgatcctgct caattcagca gtgaaagttt 350

Val Glu Thr Arg Gln Gln

80

tttgggtttt gttctgtgtt gtgttatatta tgcttttcca gaatcaattt ctgtactgga 410

ttgagtatta aaaatgtgga gctaaaggtt gggagacctg atgcctttgt tactcgagta 470

atcacaagta gatactgggc ttgtaatagc gtgataattg tgccttgctc ttgcctcatt 530

gactacgaat cagttatgtg attagacaat gttaatctcc aaaaaaaaaa aaaaaaaaaa 590

aa 592

<210> 32

<211> 82

<212> PRT

<213> Avicennia marina

<400> 32

Met Gln Asn Glu Glu Gly Gln Asn Met Asp Leu Tyr Ile Pro Arg Lys

1 5 10 15

Cys Ser Ala Thr Asn Arg Leu Ile Thr Ser Lys Asp His Ala Ser Val

20 25 30

Gln Ile Asn Val Gly His Leu Asp Glu Asn Gly Arg Tyr Thr Gly Gln

35 40 45

Tyr Ser Thr Phe Ala Leu Cys Gly Phe Ile Arg Ala Gln Gly Asp Ala

50 55 60

Asp Ser Ala Leu Asp Arg Leu Trp Gln Lys Lys Lys Val Glu Thr Arg

65 70 75 80

Gln Gln

<210> 33

<211> 1806

<212> DNA

<213> *Avicennia marina*

<220>

<221> CDS

<222> (362)..(1552)

<400> 33

tgtgaaggta aagtctacag catatttcgc gccgctcggt tgattacgtg ttgcttttat 60

ttgggaattt gatagcgctg agtagccgat gccgctggag ggtattgttg attttaggaa 120

tacgggtttg tttgattcgc agttttactg tctctagggt tgggccctga ggcttctggg 180

atttgggatt taatcgctga tcgaacagtt tcctggagaa aatactccta gtgcgcatat 240

atctgatttg ctgacgagaa attgatacac ggttatgcga ttgagttttg tttgcgcaa 300

agatactccg agtgctcgct agatgtggat aatccggagg gctgtttcga tgagatgagg 360

g atg tta tca ggg tta atg aac ttc ctg tgg gcc tgt ttt cgg cca agg 409

Met Leu Ser Gly Leu Met Asn Phe Leu Trp Ala Cys Phe Arg Pro Arg

1

5

10

15

gcg gat cga agt gtt cac acg ggt tca gat gca ggc ggt cgt cag gat 457

Ala Asp Arg Ser Val His Thr Gly Ser Asp Ala Gly Gly Arg Gln Asp

20

25

30

ggg ctt tta tgg tat aag gac ttg ggg caa cat atc aat gga gag ttt 505

Gly Leu Leu Trp Tyr Lys Asp Leu Gly Gln His Ile Asn Gly Glu Phe

35

40

45

tca atg gct gta gtt caa gca aat aac tta cta gag gat cag agt caa 553

Ser Met Ala Val Val Gln Ala Asn Asn Leu Leu Glu Asp Gln Ser Gln

50	55	60	
ctt gaa tct ggt tgc ctg agc ttg agt gat tca gga caa tat ggc act Leu Glu Ser Gly Cys Leu Ser Leu Ser Asp Ser Gly Gln Tyr Gly Thr			601
65	70	75	80
ttt gtg ggg att tat gat gga cat gga ggt cct gag acc tct cgg ttt Phe Val Gly Ile Tyr Asp Gly His Gly Gly Pro Glu Thr Ser Arg Phe			649
	85	90	95
atc aat gac cat ctc ttc caa cat ata aag aga ttc aca gct gag cat Ile Asn Asp His Leu Phe Gln His Ile Lys Arg Phe Thr Ala Glu His			697
	100	105	110
caa tca atg tca gct gag gtc att cac aag gcc att caa gcg act gaa Gln Ser Met Ser Ala Glu Val Ile His Lys Ala Ile Gln Ala Thr Glu			745
	115	120	125
gaa ggt ttt ttc tcg gtt gtt agc aga caa tgg tcc atg caa cca cag Glu Gly Phe Phe Ser Val Val Ser Arg Gln Trp Ser Met Gln Pro Gln			793
	130	135	140
att gca gca gtt ggc tct tgc tgc ctt gtt ggt gtc atc tgt agt ggc Ile Ala Ala Val Gly Ser Cys Cys Leu Val Gly Val Ile Cys Ser Gly			841
145	150	155	160
act ctt tat gtt tcc aac ctt ggt gat tcc cgt gct gtt ctt ggg acg Thr Leu Tyr Val Ser Asn Leu Gly Asp Ser Arg Ala Val Leu Gly Thr			889
	165	170	175
ctt tcc aag gct aca ggg gaa gta cag gct act caa ctc tca aca gag Leu Ser Lys Ala Thr Gly Glu Val Gln Ala Thr Gln Leu Ser Thr Glu			937
	180	185	190
cat aat gca agt ttt gag tct gtg aga cgg gaa ctg cag tct ctg cac His Asn Ala Ser Phe Glu Ser Val Arg Arg Glu Leu Gln Ser Leu His			985

195	200	205	
cca gat gac tca cag att gtg gtt cta aag cat aat gta tgg cga gtg			1033
Pro Asp Asp Ser Gln Ile Val Val Leu Lys His Asn Val Trp Arg Val			
210	215	220	
aag ggt ctt ata cag atc tca aga tca att gga gat gtg tat ttg aaa			1081
Lys Gly Leu Ile Gln Ile Ser Arg Ser Ile Gly Asp Val Tyr Leu Lys			
225	230	235	240
aag gct gaa ttc aac agg gag cct cta tat cag aaa ttt cga ctt cgt			1129
Lys Ala Glu Phe Asn Arg Glu Pro Leu Tyr Gln Lys Phe Arg Leu Arg			
	245	250	255
gaa gct ttc aaa aga cca att ttg agc tca gaa cca gaa act act gtg			1177
Glu Ala Phe Lys Arg Pro Ile Leu Ser Ser Glu Pro Glu Thr Thr Val			
	260	265	270
cac cag ctg ctg cct cat gat caa ttc att atc ttc gca tca gat ggc			1225
His Gln Leu Leu Pro His Asp Gln Phe Ile Ile Phe Ala Ser Asp Gly			
	275	280	285
ctt tgg gag cac ctt tcc aac caa gaa gca gtt gat ctt gtt cag aaa			1273
Leu Trp Glu His Leu Ser Asn Gln Glu Ala Val Asp Leu Val Gln Lys			
290	295	300	
cat cca cac aat ggg att gct aga aga tta gta aaa gca gct ttg caa			1321
His Pro His Asn Gly Ile Ala Arg Arg Leu Val Lys Ala Ala Leu Gln			
305	310	315	320
gag gca gca aag aaa agg gaa atg agg tac tcg gat ttg aag aaa att			1369
Glu Ala Ala Lys Lys Arg Glu Met Arg Tyr Ser Asp Leu Lys Lys Ile			
	325	330	335
gac cgt ggg gtt cgc cgt cat ttc cat gat gac atc act gtt gtg gtg			1417
Asp Arg Gly Val Arg Arg His Phe His Asp Asp Ile Thr Val Val Val			

340	345	350	
gtg ttt ctt gac tca cac ctt gtg agc cgg gct agc tca gtc cgg ggc			1465
Val Phe Leu Asp Ser His Leu Val Ser Arg Ala Ser Ser Val Arg Gly			
355	360	365	
cca aac atc tcc gtg aaa ggt ggc ggc atc agt ctg cct ccc aat gct			1513
Pro Asn Ile Ser Val Lys Gly Gly Gly Ile Ser Leu Pro Pro Asn Ala			
370	375	380	
ctt gca cct tgt gcc aca cca acg gag cca gtc cca aat tgatactgct			1562
Leu Ala Pro Cys Ala Thr Pro Thr Glu Pro Val Pro Asn			
385	390	395	
gtctcttcta atgttatctc cegttagtcc tgttgtacta ttgttatgtg aatacaggta			1622
gcttcttaac ggataacagc ggcccttgaa ttctttaatc catactgtaa cttttaaccg			1682
gagactatta cttggcatag tttcaatgcc caagggatac atagactggg acaagccatc			1742
ttggcgggtga caatcatcat agttaagttt tctgggcata tctttcaaaa aaaaaaaaaa			1802
aaaa			1806

<210> 34

<211> 397

<212> PRT

<213> *Avicennia marina*

<400> 34

Met	Leu	Ser	Gly	Leu	Met	Asn	Phe	Leu	Trp	Ala	Cys	Phe	Arg	Pro	Arg
1				5						10					15

Ala	Asp	Arg	Ser	Val	His	Thr	Gly	Ser	Asp	Ala	Gly	Gly	Arg	Gln	Asp
				20						25					30

Gly Leu Leu Trp Tyr Lys Asp Leu Gly Gln His Ile Asn Gly Glu Phe
35 40 45

Ser Met Ala Val Val Gln Ala Asn Asn Leu Leu Glu Asp Gln Ser Gln
50 55 60

Leu Glu Ser Gly Cys Leu Ser Leu Ser Asp Ser Gly Gln Tyr Gly Thr
65 70 75 80

Phe Val Gly Ile Tyr Asp Gly His Gly Gly Pro Glu Thr Ser Arg Phe
85 90 95

Ile Asn Asp His Leu Phe Gln His Ile Lys Arg Phe Thr Ala Glu His
100 105 110

Gln Ser Met Ser Ala Glu Val Ile His Lys Ala Ile Gln Ala Thr Glu
115 120 125

Glu Gly Phe Phe Ser Val Val Ser Arg Gln Trp Ser Met Gln Pro Gln
130 135 140

Ile Ala Ala Val Gly Ser Cys Cys Leu Val Gly Val Ile Cys Ser Gly
145 150 155 160

Thr Leu Tyr Val Ser Asn Leu Gly Asp Ser Arg Ala Val Leu Gly Thr
165 170 175

Leu Ser Lys Ala Thr Gly Glu Val Gln Ala Thr Gln Leu Ser Thr Glu
180 185 190

His Asn Ala Ser Phe Glu Ser Val Arg Arg Glu Leu Gln Ser Leu His
195 200 205

Pro Asp Asp Ser Gln Ile Val Val Leu Lys His Asn Val Trp Arg Val
210 215 220

Lys Gly Leu Ile Gln Ile Ser Arg Ser Ile Gly Asp Val Tyr Leu Lys
225 230 235 240

Lys Ala Glu Phe Asn Arg Glu Pro Leu Tyr Gln Lys Phe Arg Leu Arg
245 250 255

Glu Ala Phe Lys Arg Pro Ile Leu Ser Ser Glu Pro Glu Thr Thr Val
260 265 270

His Gln Leu Leu Pro His Asp Gln Phe Ile Ile Phe Ala Ser Asp Gly
275 280 285

Leu Trp Glu His Leu Ser Asn Gln Glu Ala Val Asp Leu Val Gln Lys
290 295 300

His Pro His Asn Gly Ile Ala Arg Arg Leu Val Lys Ala Ala Leu Gln
305 310 315 320

Glu Ala Ala Lys Lys Arg Glu Met Arg Tyr Ser Asp Leu Lys Lys Ile
325 330 335

Asp Arg Gly Val Arg Arg His Phe His Asp Asp Ile Thr Val Val Val
340 345 350

Val Phe Leu Asp Ser His Leu Val Ser Arg Ala Ser Ser Val Arg Gly
355 360 365

Pro Asn Ile Ser Val Lys Gly Gly Gly Ile Ser Leu Pro Pro Asn Ala
370 375 380

Leu Ala Pro Cys Ala Thr Pro Thr Glu Pro Val Pro Asn
385 390 395

<210> 35

<211> 743

<212> DNA

<213> Mesembryanthemum crystallinum

<220>

<221> CDS

<222> (1)..(420)

<400> 35

cct	gag	cta	gca	cct	aaa	gat	ggg	gat	ttc	cgt	ttc	aat	atc	tct	gag	48
Pro	Glu	Leu	Ala	Pro	Lys	Asp	Gly	Asp	Phe	Arg	Phe	Asn	Ile	Ser	Glu	
1				5					10					15		

ctt	gaa	gct	atg	cta	cca	gct	gga	act	gta	gat	cat	gct	gtt	gaa	agg	96
Leu	Glu	Ala	Met	Leu	Pro	Ala	Gly	Thr	Val	Asp	His	Ala	Val	Glu	Arg	
			20					25						30		

att	tat	caa	gag	atg	ccg	cgg	tgg	gaa	gag	act	gtt	tta	ggt	tcc	agg	144
Ile	Tyr	Gln	Glu	Met	Pro	Arg	Trp	Glu	Glu	Thr	Val	Leu	Gly	Ser	Arg	
		35				40						45				

agc	aga	tat	gag	cat	gtc	att	cag	gca	ctt	gca	gat	aaa	tac	cct	tca	192
Ser	Arg	Tyr	Glu	His	Val	Ile	Gln	Ala	Leu	Ala	Asp	Lys	Tyr	Pro	Ser	
	50					55						60				

gaa	aat	ttg	ttg	cta	gtt	acg	cat	ggt	gaa	ggt	gtt	ggg	act	tca	gtt	240
Glu	Asn	Leu	Leu	Leu	Val	Thr	His	Gly	Glu	Gly	Val	Gly	Thr	Ser	Val	
65					70					75				80		

gca	acg	ttt	ttg	aaa	ggc	gct	gtt	gtt	tat	gaa	gta	aag	tat	tgt	gct	288
Ala	Thr	Phe	Leu	Lys	Gly	Ala	Val	Val	Tyr	Glu	Val	Lys	Tyr	Cys	Ala	
			85					90						95		

tat	tca	caa	gca	aca	aga	cgc	atc	agc	tat	gga	gaa	ggc	gag	tca	ttt	336
Tyr	Ser	Gln	Ala	Thr	Arg	Arg	Ile	Ser	Tyr	Gly	Glu	Gly	Glu	Ser	Phe	

100	105	110	
act gct ggt acc ttt cag ttg gtc act gcc tca gac caa acc ggt att			384
Thr Ala Gly Thr Phe Gln Leu Val Thr Ala Ser Asp Gln Thr Gly Ile			
115	120	125	
ggt tac tac aca tct agc agc ttg tct gat ggt gta tgacttatcg			430
Gly Tyr Tyr Thr Ser Ser Ser Leu Ser Asp Gly Val			
130	135	140	
gaactcccgga gtttctgcat tctgaaaggt gctttttgat ttccgaataa ttcttcaa			490
ccacatgtca gaagatccat tcttttaggtc agatgtctat ctactgctcc cagccttgag			550
ctgctcatgg gtattgggtgc ccttctat ttaggtagag tctttgagta agccttgcca			610
catcaaggcc tcagattatt gaatgtacaa cagaataggt thtagcttca ttggctagta			670
cagtgacctc tttcatgggt ctgaaacatc aatataaagg tttgaatggc aaaaaaaaaa			730
aaaaaaaaaa aaa			743

<210> 36

<211> 140

<212> PRT

<213> Mesembryanthemum crystallinum

<400> 36

Pro	Glu	Leu	Ala	Pro	Lys	Asp	Gly	Asp	Phe	Arg	Phe	Asn	Ile	Ser	Glu
1				5					10					15	

Leu	Glu	Ala	Met	Leu	Pro	Ala	Gly	Thr	Val	Asp	His	Ala	Val	Glu	Arg
			20					25						30	

Ile	Tyr	Gln	Glu	Met	Pro	Arg	Trp	Glu	Glu	Thr	Val	Leu	Gly	Ser	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35	40	45
Ser Arg Tyr Glu His Val Ile Gln Ala Leu Ala Asp Lys Tyr Pro Ser		
50	55	60
Glu Asn Leu Leu Leu Val Thr His Gly Glu Gly Val Gly Thr Ser Val		
65	70	75
Ala Thr Phe Leu Lys Gly Ala Val Val Tyr Glu Val Lys Tyr Cys Ala		
85	90	95
Tyr Ser Gln Ala Thr Arg Arg Ile Ser Tyr Gly Glu Gly Glu Ser Phe		
100	105	110
Thr Ala Gly Thr Phe Gln Leu Val Thr Ala Ser Asp Gln Thr Gly Ile		
115	120	125
Gly Tyr Tyr Thr Ser Ser Ser Leu Ser Asp Gly Val		
130	135	140

<210> 37

<211> 348

<212> DNA

<213> Sueada japonica

<220>

<221> CDS

<222> (1)..(246)

<400> 37

atc att gct ccc cta gct att ggt ttg atc gtt ggt gcc aac atc tta	48
Ile Ile Ala Pro Leu Ala Ile Gly Leu Ile Val Gly Ala Asn Ile Leu	
1	5
	10
	15

gcc gga ggt gca ttt gat ggt gcc tca atg aac cct gcc gtc tct ttt 96
 Ala Gly Gly Ala Phe Asp Gly Ala Ser Met Asn Pro Ala Val Ser Phe
 20 25 30

ggc ccc gcc gtg gtt agc tgg agc tgg gcc aac cac tgg gtc tac tgg 144
 Gly Pro Ala Val Val Ser Trp Ser Trp Ala Asn His Trp Val Tyr Trp
 35 40 45

gca ggc cca ctc att ggt ggt gga ctt gct ggt ctc gtt tat gag ttt 192
 Ala Gly Pro Leu Ile Gly Gly Gly Leu Ala Gly Leu Val Tyr Glu Phe
 50 55 60

atc ttt att ggt cac caa gag cca gct tcc gct gac tac cag aga ctc 240
 Ile Phe Ile Gly His Gln Glu Pro Ala Ser Ala Asp Tyr Gln Arg Leu
 65 70 75 80

tct gct taagaatttt aattctttgc cctagggaaa aatgtttcat gcatgtattt 296
 Ser Ala

tggtattttg ttgggtctaa aattttatga agggaaaaaa aaaaaaaaaa aa 348

<210> 38

<211> 82

<212> PRT

<213> Sueada japonica

<400> 38

Ile Ile Ala Pro Leu Ala Ile Gly Leu Ile Val Gly Ala Asn Ile Leu
 1 5 10 15

Ala Gly Gly Ala Phe Asp Gly Ala Ser Met Asn Pro Ala Val Ser Phe
 20 25 30

Gly Pro Ala Val Val Ser Trp Ser Trp Ala Asn His Trp Val Tyr Trp
 35 40 45

Ala Gly Pro Leu Ile Gly Gly Gly Leu Ala Gly Leu Val Tyr Glu Phe
50 55 60

Ile Phe Ile Gly His Gln Glu Pro Ala Ser Ala Asp Tyr Gln Arg Leu
65 70 75 80

Ser Ala

<210> 39

<211> 1602

<212> DNA

<213> Sueada japonica

<220>

<221> CDS

<222> (1)..(1419)

<400> 39

cac acc gtt gat tta acc att gaa gct atg atg ctc gat tct caa gct 48
His Thr Val Asp Leu Thr Ile Glu Ala Met Met Leu Asp Ser Gln Ala
1 5 10 15

tct gat ctt gac aaa gaa gaa cgt cct gag att ctt tca atg ctt ccg 96
Ser Asp Leu Asp Lys Glu Glu Arg Pro Glu Ile Leu Ser Met Leu Pro
20 25 30

cct ctt gaa gga aaa tgc ctc ttg gaa ctt ggg gct ggt att ggt cgt 144
Pro Leu Glu Gly Lys Cys Leu Leu Glu Leu Gly Ala Gly Ile Gly Arg
35 40 45

ttt act ggt gaa ttg gct gag aaa gct ggc cag gtt att gct ctg gat 192
Phe Thr Gly Glu Leu Ala Glu Lys Ala Gly Gln Val Ile Ala Leu Asp

50	55	60	
ttc att gag agt gct atc aag aag aat gaa gta atc aat ggg cac tac			240
Phe Ile Glu Ser Ala Ile Lys Lys Asn Glu Val Ile Asn Gly His Tyr			
65	70	75	80
aaa aat gtc aag ttt atg tgt gct gat gtg act tct ccc act ctc agt			288
Lys Asn Val Lys Phe Met Cys Ala Asp Val Thr Ser Pro Thr Leu Ser			
	85	90	95
ttc cca cca cat tca ttg gat gtg ata ttc tcc aat tgg tta ctc atg			336
Phe Pro Pro His Ser Leu Asp Val Ile Phe Ser Asn Trp Leu Leu Met			
	100	105	110
tat ctt tct gat gaa gag gtg gaa aat ttg gtt gaa aga atg ttg aaa			384
Tyr Leu Ser Asp Glu Glu Val Glu Asn Leu Val Glu Arg Met Leu Lys			
	115	120	125
tgg ttg aag cca ggg ggt tac att ttc ttc aga gaa tct tgt ttc cat			432
Trp Leu Lys Pro Gly Gly Tyr Ile Phe Phe Arg Glu Ser Cys Phe His			
	130	135	140
caa tct ggg gat cac aaa cgc aaa agc aat ccc acc cac tac cgt gaa			480
Gln Ser Gly Asp His Lys Arg Lys Ser Asn Pro Thr His Tyr Arg Glu			
	145	150	155
cct agg ttc tac act aag gcc ttc aaa gag tgt cat ttg caa gat gga			528
Pro Arg Phe Tyr Thr Lys Ala Phe Lys Glu Cys His Leu Gln Asp Gly			
	165	170	175
tct gga aac tct tat gag ctc tcc cta ctt agc tgc aaa tgt att gga			576
Ser Gly Asn Ser Tyr Glu Leu Ser Leu Leu Ser Cys Lys Cys Ile Gly			
	180	185	190
gct tat gtc aga aac aag aaa aac cag aac cag att agt tgg ttg tgg			624
Ala Tyr Val Arg Asn Lys Lys Asn Gln Asn Gln Ile Ser Trp Leu Trp			

195	200	205	
caa aaa gtt gat tct aag gat gat aag ggg ttc cag cga ttt ctg gat			672
Gln Lys Val Asp Ser Lys Asp Asp Lys Gly Phe Gln Arg Phe Leu Asp			
210	215	220	
act agc cag tac aag tgt aat agc att ctg cga tat gag cgt gta ttt			720
Thr Ser Gln Tyr Lys Cys Asn Ser Ile Leu Arg Tyr Glu Arg Val Phe			
225	230	235	240
ggc cct ggt tat gtt agc act gga gga tat gaa acc acc aaa gag ttt			768
Gly Pro Gly Tyr Val Ser Thr Gly Gly Tyr Glu Thr Thr Lys Glu Phe			
245	250	255	
gtg tca atg ctg gac ttg aag cct ggc cag aag gtc ctg gat gtt ggt			816
Val Ser Met Leu Asp Leu Lys Pro Gly Gln Lys Val Leu Asp Val Gly			
260	265	270	
tgt gga att ggt gga ggt gac ttt tac atg gcg gag acc ttt gat gtt			864
Cys Gly Ile Gly Gly Gly Asp Phe Tyr Met Ala Glu Thr Phe Asp Val			
275	280	285	
gag gtt gtt gga ttt gat ctc tcc gtt aat atg att tcc ttt gcc ctt			912
Glu Val Val Gly Phe Asp Leu Ser Val Asn Met Ile Ser Phe Ala Leu			
290	295	300	
gag cgt tct att ggg ctt aaa tgt gct gtt gag ttt gag gta gca gat			960
Glu Arg Ser Ile Gly Leu Lys Cys Ala Val Glu Phe Glu Val Ala Asp			
305	310	315	320
tgc acc aag ata aac tac cct gat aac tct ttt gat gtc atc tat agc			1008
Cys Thr Lys Ile Asn Tyr Pro Asp Asn Ser Phe Asp Val Ile Tyr Ser			
325	330	335	
cgt gac acc att ctg cat att cag gac aag cct gcg ttg ttt aga tcc			1056
Arg Asp Thr Ile Leu His Ile Gln Asp Lys Pro Ala Leu Phe Arg Ser			

340	345	350	
ttc tac aaa tgg ttg aag cca gga ggt aaa gtt cta atc agt gat tac	1104		
Phe Tyr Lys Trp Leu Lys Pro Gly Gly Lys Val Leu Ile Ser Asp Tyr			
355	360	365	
tgc aag aaa gct ggt cca ccc tca cct gaa ttc gcc gct tac att aag	1152		
Cys Lys Lys Ala Gly Pro Pro Ser Pro Glu Phe Ala Ala Tyr Ile Lys			
370	375	380	
cag agg gga tat gat ctc cat gat gta aag gaa tat ggg cag atg ctt	1200		
Gln Arg Gly Tyr Asp Leu His Asp Val Lys Glu Tyr Gly Gln Met Leu			
385	390	395	400
aaa gat gct gga ttt gtt gat gtt ctt gcc gag gat aga act gag cag	1248		
Lys Asp Ala Gly Phe Val Asp Val Leu Ala Glu Asp Arg Thr Glu Gln			
405	410	415	
ttc att cga gtt cta cgg aag gaa cta gag act gtt gag aag gaa aag	1296		
Phe Ile Arg Val Leu Arg Lys Glu Leu Glu Thr Val Glu Lys Glu Lys			
420	425	430	
gat gtg ttc att agt gat ttc tct gag gag gat tac aat gac att gtt	1344		
Asp Val Phe Ile Ser Asp Phe Ser Glu Glu Asp Tyr Asn Asp Ile Val			
435	440	445	
gga ggt tgg aat gat aag ttg cgg agg act gcc aag ggt gag caa cga	1392		
Gly Gly Trp Asn Asp Lys Leu Arg Arg Thr Ala Lys Gly Glu Gln Arg			
450	455	460	
tgg ggt ctg ttc gtt gcc aag aag aag tgaagaatca gttgccgcac	1439		
Trp Gly Leu Phe Val Ala Lys Lys Lys			
465	470		
tggcactgtc gatttcctag tattaatctt caatgttttc atgtaatgta cttctacatg	1499		

taaaattgcc aataagttgc atttcgcaga ctgtaagatg attaatacata ttttatcttt 1559

taattaatca tggatttatg caaaaaaaaa aaaaaaaaaa aaa 1602

<210> 40

<211> 473

<212> PRT

<213> Sueada japonica

<400> 40

His	Thr	Val	Asp	Leu	Thr	Ile	Glu	Ala	Met	Met	Leu	Asp	Ser	Gln	Ala
1				5					10					15	

Ser	Asp	Leu	Asp	Lys	Glu	Glu	Arg	Pro	Glu	Ile	Leu	Ser	Met	Leu	Pro
			20					25					30		

Pro	Leu	Glu	Gly	Lys	Cys	Leu	Leu	Glu	Leu	Gly	Ala	Gly	Ile	Gly	Arg
			35					40					45		

Phe	Thr	Gly	Glu	Leu	Ala	Glu	Lys	Ala	Gly	Gln	Val	Ile	Ala	Leu	Asp
	50						55					60			

Phe	Ile	Glu	Ser	Ala	Ile	Lys	Lys	Asn	Glu	Val	Ile	Asn	Gly	His	Tyr
65					70				75					80	

Lys	Asn	Val	Lys	Phe	Met	Cys	Ala	Asp	Val	Thr	Ser	Pro	Thr	Leu	Ser
				85					90					95	

Phe	Pro	Pro	His	Ser	Leu	Asp	Val	Ile	Phe	Ser	Asn	Trp	Leu	Leu	Met
			100					105					110		

Tyr	Leu	Ser	Asp	Glu	Glu	Val	Glu	Asn	Leu	Val	Glu	Arg	Met	Leu	Lys
			115					120				125			

Trp	Leu	Lys	Pro	Gly	Gly	Tyr	Ile	Phe	Phe	Arg	Glu	Ser	Cys	Phe	His
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

130	135	140	
Gln Ser Gly Asp His Lys Arg Lys Ser Asn Pro Thr His Tyr Arg Glu			
145	150	155	160
Pro Arg Phe Tyr Thr Lys Ala Phe Lys Glu Cys His Leu Gln Asp Gly			
	165	170	175
Ser Gly Asn Ser Tyr Glu Leu Ser Leu Leu Ser Cys Lys Cys Ile Gly			
	180	185	190
Ala Tyr Val Arg Asn Lys Lys Asn Gln Asn Gln Ile Ser Trp Leu Trp			
	195	200	205
Gln Lys Val Asp Ser Lys Asp Asp Lys Gly Phe Gln Arg Phe Leu Asp			
210	215	220	
Thr Ser Gln Tyr Lys Cys Asn Ser Ile Leu Arg Tyr Glu Arg Val Phe			
225	230	235	240
Gly Pro Gly Tyr Val Ser Thr Gly Gly Tyr Glu Thr Thr Lys Glu Phe			
	245	250	255
Val Ser Met Leu Asp Leu Lys Pro Gly Gln Lys Val Leu Asp Val Gly			
	260	265	270
Cys Gly Ile Gly Gly Gly Asp Phe Tyr Met Ala Glu Thr Phe Asp Val			
	275	280	285
Glu Val Val Gly Phe Asp Leu Ser Val Asn Met Ile Ser Phe Ala Leu			
290	295	300	
Glu Arg Ser Ile Gly Leu Lys Cys Ala Val Glu Phe Glu Val Ala Asp			
305	310	315	320
Cys Thr Lys Ile Asn Tyr Pro Asp Asn Ser Phe Asp Val Ile Tyr Ser			

	325		330		335
Arg Asp Thr Ile Leu His Ile Gln Asp Lys Pro Ala Leu Phe Arg Ser					
	340		345		350
Phe Tyr Lys Trp Leu Lys Pro Gly Gly Lys Val Leu Ile Ser Asp Tyr					
	355		360		365
Cys Lys Lys Ala Gly Pro Pro Ser Pro Glu Phe Ala Ala Tyr Ile Lys					
	370		375		380
Gln Arg Gly Tyr Asp Leu His Asp Val Lys Glu Tyr Gly Gln Met Leu					
385		390		395	400
Lys Asp Ala Gly Phe Val Asp Val Leu Ala Glu Asp Arg Thr Glu Gln					
	405		410		415
Phe Ile Arg Val Leu Arg Lys Glu Leu Glu Thr Val Glu Lys Glu Lys					
	420		425		430
Asp Val Phe Ile Ser Asp Phe Ser Glu Glu Asp Tyr Asn Asp Ile Val					
	435		440		445
Gly Gly Trp Asn Asp Lys Leu Arg Arg Thr Ala Lys Gly Glu Gln Arg					
	450		455		460
Trp Gly Leu Phe Val Ala Lys Lys Lys					
465		470			

<210> 41

<211> 1251

<212> DNA

<213> Salsola komarovii

<220>

<221> CDS

<222> (1).. (933)

<400> 41

cag cca ttt ggc aca att aat gga tca ctt cgt gtt act gta caa ggt 48
Gln Pro Phe Gly Thr Ile Asn Gly Ser Leu Arg Val Thr Val Gln Gly
1 5 10 15

gag gtc att gaa caa tct ttt gga gag gag cac ttg tgt ttt aga aca 96
Glu Val Ile Glu Gln Ser Phe Gly Glu Glu His Leu Cys Phe Arg Thr
20 25 30

tta cag cgg tac aca gct gcc aca ctt gag cat gga atg cat cca cca 144
Leu Gln Arg Tyr Thr Ala Ala Thr Leu Glu His Gly Met His Pro Pro
35 40 45

atc tct cct aaa cca gaa tgg cgt gca ctt ttg gac gag atg gct gtt 192
Ile Ser Pro Lys Pro Glu Trp Arg Ala Leu Leu Asp Glu Met Ala Val
50 55 60

gtt gcc acc aag gaa tac cgc tct gtt gtt ttt cat gag cct cgc ttt 240
Val Ala Thr Lys Glu Tyr Arg Ser Val Val Phe His Glu Pro Arg Phe
65 70 75 80

gtc gag tac ttc cgc agt gct aca cca gag aca gag tat ggg cgt atg 288
Val Glu Tyr Phe Arg Ser Ala Thr Pro Glu Thr Glu Tyr Gly Arg Met
85 90 95

aat att gga agc cgt cct gca aag aga aag cca gga gga gga att gaa 336
Asn Ile Gly Ser Arg Pro Ala Lys Arg Lys Pro Gly Gly Gly Ile Glu
100 105 110

act ctg cgt gca att cct tgg ata ttt tcg tgg aca caa acc agg ttt 384
Thr Leu Arg Ala Ile Pro Trp Ile Phe Ser Trp Thr Gln Thr Arg Phe
115 120 125

cat tta cct gtg tgg ctt ggg gtt gga gca gct ttt aag cat gcc ctt	432
His Leu Pro Val Trp Leu Gly Val Gly Ala Ala Phe Lys His Ala Leu	
130 135 140	
 gac aag gac att aag aat ctt tcg ata ctc aag gcc atg tat aat gag	480
Asp Lys Asp Ile Lys Asn Leu Ser Ile Leu Lys Ala Met Tyr Asn Glu	
145 150 155 160	
 tgg ccg ttc ttc aga gtg act att gat ctc tta gaa atg gtt ttc act	528
Trp Pro Phe Phe Arg Val Thr Ile Asp Leu Leu Glu Met Val Phe Thr	
165 170 175	
 aaa gga gac cct gga att gct gct tta tat gac aag ctt ctg gtg gca	576
Lys Gly Asp Pro Gly Ile Ala Ala Leu Tyr Asp Lys Leu Leu Val Ala	
180 185 190	
 gag gat ttg aag ccc ttt ggg gaa aag ttg agg aaa agt ttc gaa gat	624
Glu Asp Leu Lys Pro Phe Gly Glu Lys Leu Arg Lys Ser Phe Glu Asp	
195 200 205	
 acc aaa ctc ctt ctc ctt aag gtt gct ggg cac aag gag tta ctg gaa	672
Thr Lys Leu Leu Leu Leu Lys Val Ala Gly His Lys Glu Leu Leu Glu	
210 215 220	
 gga gat cct tac ttg aaa cag aga ctc cga ctt cgt gat cct tac att	720
Gly Asp Pro Tyr Leu Lys Gln Arg Leu Arg Leu Arg Asp Pro Tyr Ile	
225 230 235 240	
 aca acc ctt aat gtt ttc caa gca tat act ctg aag cgg atc cgt gat	768
Thr Thr Leu Asn Val Phe Gln Ala Tyr Thr Leu Lys Arg Ile Arg Asp	
245 250 255	
 ccc aat ttc cat gta gct gaa ggg cca cac tta tcc aag gaa gta ttg	816
Pro Asn Phe His Val Ala Glu Gly Pro His Leu Ser Lys Glu Val Leu	
260 265 270	

gaa tca aac aat gct gag ctt gtg aag ctc aat cct act agt gag tat 864
 Glu Ser Asn Asn Ala Glu Leu Val Lys Leu Asn Pro Thr Ser Glu Tyr
 275 280 285

cct cct ggc ctt gag gac acc ctt atc ttg acc atg aag ggt att gct 912
 Pro Pro Gly Leu Glu Asp Thr Leu Ile Leu Thr Met Lys Gly Ile Ala
 290 295 300

gct ggc atg cag aac acc ggt taactgacac gtgttgacag tctattgcaa 963
 Ala Gly Met Gln Asn Thr Gly
 305 310

ctattcctca actccttctg gtttggggat cgggctcgg agatagccat cgttggtgat 1023

gtgctgtatg agcacctaataa tgtattcaaaa gtctgtatatt caagtctatt gtatttgtat 1083

tttgttcttc tgtatgtttt tgttatttct acttatgggtt gggttggtgc acttgtgact 1143

aatacccgac tgtgtaataa atgggtgttg tactgatgaa cagtttgttt tcttctacgt 1203

gagttatatt gatgagttaa tcttttatta aaaaaaaaaa aaaaaaaaaa 1251

<210> 42

<211> 311

<212> PRT

<213> Salsola komarovii

<400> 42

Gln Pro Phe Gly Thr Ile Asn Gly Ser Leu Arg Val Thr Val Gln Gly
 1 5 10 15

Glu Val Ile Glu Gln Ser Phe Gly Glu Glu His Leu Cys Phe Arg Thr
 20 25 30

Leu Gln Arg Tyr Thr Ala Ala Thr Leu Glu His Gly Met His Pro Pro
35 40 45

Ile Ser Pro Lys Pro Glu Trp Arg Ala Leu Leu Asp Glu Met Ala Val
50 55 60

Val Ala Thr Lys Glu Tyr Arg Ser Val Val Phe His Glu Pro Arg Phe
65 70 75 80

Val Glu Tyr Phe Arg Ser Ala Thr Pro Glu Thr Glu Tyr Gly Arg Met
85 90 95

Asn Ile Gly Ser Arg Pro Ala Lys Arg Lys Pro Gly Gly Gly Ile Glu
100 105 110

Thr Leu Arg Ala Ile Pro Trp Ile Phe Ser Trp Thr Gln Thr Arg Phe
115 120 125

His Leu Pro Val Trp Leu Gly Val Gly Ala Ala Phe Lys His Ala Leu
130 135 140

Asp Lys Asp Ile Lys Asn Leu Ser Ile Leu Lys Ala Met Tyr Asn Glu
145 150 155 160

Trp Pro Phe Phe Arg Val Thr Ile Asp Leu Leu Glu Met Val Phe Thr
165 170 175

Lys Gly Asp Pro Gly Ile Ala Ala Leu Tyr Asp Lys Leu Leu Val Ala
180 185 190

Glu Asp Leu Lys Pro Phe Gly Glu Lys Leu Arg Lys Ser Phe Glu Asp
195 200 205

Thr Lys Leu Leu Leu Leu Lys Val Ala Gly His Lys Glu Leu Leu Glu
210 215 220

Gly Asp Pro Tyr Leu Lys Gln Arg Leu Arg Leu Arg Asp Pro Tyr Ile
 225 230 235 240

Thr Thr Leu Asn Val Phe Gln Ala Tyr Thr Leu Lys Arg Ile Arg Asp
 245 250 255

Pro Asn Phe His Val Ala Glu Gly Pro His Leu Ser Lys Glu Val Leu
 260 265 270

Glu Ser Asn Asn Ala Glu Leu Val Lys Leu Asn Pro Thr Ser Glu Tyr
 275 280 285

Pro Pro Gly Leu Glu Asp Thr Leu Ile Leu Thr Met Lys Gly Ile Ala
 290 295 300

Ala Gly Met Gln Asn Thr Gly
 305 310

<210> 43

<211> 637

<212> DNA

<213> Avicennia marina

<220>

<221> CDS

<222> (1)..(339)

<400> 43

caa tac ttg gta aat gaa gtg aag aaa act gtt cag ggg cgt gct caa 48
 Gln Tyr Leu Val Asn Glu Val Lys Lys Thr Val Gln Gly Arg Ala Gln
 1 5 10 15

ctt ggt gtg gaa gca ttt gct gat gcg ctt ctt gtg gtt cca aag acg 96
 Leu Gly Val Glu Ala Phe Ala Asp Ala Leu Leu Val Val Pro Lys Thr

20	25	30	
ctt gcc gag aac tct ggc ctt gat acc cag gat ttg att att gaa ctt			144
Leu Ala Glu Asn Ser Gly Leu Asp Thr Gln Asp Leu Ile Ile Glu Leu			
35	40	45	
acg gga gaa tat gaa aaa ggg aat gtg gta gga ctt aat cta cac aca			192
Thr Gly Glu Tyr Glu Lys Gly Asn Val Val Gly Leu Asn Leu His Thr			
50	55	60	
gga gaa cct ata gat cct caa atg gag ggt atc ttt gac aat tat tcc			240
Gly Glu Pro Ile Asp Pro Gln Met Glu Gly Ile Phe Asp Asn Tyr Ser			
65	70	75	80
gtg aag cgt cag atc ata aac tca ggc ccc gtt att gca tct cag ctg			288
Val Lys Arg Gln Ile Ile Asn Ser Gly Pro Val Ile Ala Ser Gln Leu			
85	90	95	
cta ctt gtc gac gag gtt att cgt gct ggt cgt aac atg cgt aaa ccg			336
Leu Leu Val Asp Glu Val Ile Arg Ala Gly Arg Asn Met Arg Lys Pro			
100	105	110	
aat tagctttcac cctagttttt gtgatgttgg tgaagatggg aattttattt			389
Asn			
aggtagggtc atggttcctt ttgtttagcc taagcactat gtattcattg ccacttgaga			449
tttgaatttt gatcatcagg cggttgaact tttgcctgt tacaaattgc accagaaatt			509
attcgacat gggtatgcat ctacttgtgt tgtacctgac ttggctaagt tatttgaaga			569
tacactctgt gctcagcaaa gaattgaaa aaaaggaatt gatttcatca aaaaaaaaaa			629
aaaaaaaaaa			637

<210> 44

<211> 113

<212> PRT

<213> Avicennia marina

<400> 44

Gln Tyr Leu Val Asn Glu Val Lys Lys Thr Val Gln Gly Arg Ala Gln

1 5 10 15

Leu Gly Val Glu Ala Phe Ala Asp Ala Leu Leu Val Val Pro Lys Thr

20 25 30

Leu Ala Glu Asn Ser Gly Leu Asp Thr Gln Asp Leu Ile Ile Glu Leu

35 40 45

Thr Gly Glu Tyr Glu Lys Gly Asn Val Val Gly Leu Asn Leu His Thr

50 55 60

Gly Glu Pro Ile Asp Pro Gln Met Glu Gly Ile Phe Asp Asn Tyr Ser

65 70 75 80

Val Lys Arg Gln Ile Ile Asn Ser Gly Pro Val Ile Ala Ser Gln Leu

85 90 95

Leu Leu Val Asp Glu Val Ile Arg Ala Gly Arg Asn Met Arg Lys Pro

100 105 110

Asn

<210> 45

<211> 741

<212> DNA

<213> Avicennia marina

<220>

<221> CDS

<222> (3)..(293)

<400> 45

aa gag atc aat tgt ctt gaa tgg gag aac ttt gct ttc cat ccc agc 47

Glu Ile Asn Cys Leu Glu Trp Glu Asn Phe Ala Phe His Pro Ser

1 5 10 15

cca ctc att gtt ctt gtt ttt gaa aga tac aac agg gca agt gat aac 95

Pro Leu Ile Val Leu Val Phe Glu Arg Tyr Asn Arg Ala Ser Asp Asn

20 25 30

tgg aaa gct ttg aag gag ttg gaa aag gcg gca gaa gtt tac tgg aag 143

Trp Lys Ala Leu Lys Glu Leu Glu Lys Ala Ala Glu Val Tyr Trp Lys

35 40 45

gca aaa gat cga ctg cct cct cgg acg gtc aag ata gat ata aac atc 191

Ala Lys Asp Arg Leu Pro Pro Arg Thr Val Lys Ile Asp Ile Asn Ile

50 55 60

gaa agg gat tta gca tat gca ctc aag gtt aaa gaa tgc ccg cag ata 239

Glu Arg Asp Leu Ala Tyr Ala Leu Lys Val Lys Glu Cys Pro Gln Ile

65 70 75

ctg ttc tta cgc gga aac agg ata tta tac aga gag aaa ggt agc cca 287

Leu Phe Leu Arg Gly Asn Arg Ile Leu Tyr Arg Glu Lys Gly Ser Pro

80 85 90 95

ttt ctc tgatattgca tgtacatcag atctttcaat ctgcaccaga accaattgag 343

Phe Leu

tttaccatca tttccagaaa ttagatcatc ggatgaattg gttcagatga tcgcgcattt 403

ctattacaat gcaaaaaagc cttcgtgcat cgatgatgca gctttctctt caccacatca 463

ctgaaggtga ggttgtcaaa tggaatccag catcagtcac tagggaggac tgaagctgta 523
 cggaggggaag tggtttaaat tcagattgga tctttgaagt gggcagtggg gattgaaacg 583
 ccaaaagttt ctgaggaata accttggttg gattttgcag tgaactgtag taactttctc 643
 gcatgtaaaa ctgactttc atcaatcaac caccaaccct tttatgtata tgaaacctat 703
 gaggttgaaa tttctagtta aaaaaaaaaa aaaaaaaaa 741

<210> 46
 <211> 97
 <212> PRT
 <213> *Avicennia marina*

<400> 46

Glu	Ile	Asn	Cys	Leu	Glu	Trp	Glu	Asn	Phe	Ala	Phe	His	Pro	Ser	Pro
1				5					10					15	

Leu	Ile	Val	Leu	Val	Phe	Glu	Arg	Tyr	Asn	Arg	Ala	Ser	Asp	Asn	Trp
			20						25					30	

Lys	Ala	Leu	Lys	Glu	Leu	Glu	Lys	Ala	Ala	Glu	Val	Tyr	Trp	Lys	Ala
			35					40						45	

Lys	Asp	Arg	Leu	Pro	Pro	Arg	Thr	Val	Lys	Ile	Asp	Ile	Asn	Ile	Glu
			50					55					60		

Arg	Asp	Leu	Ala	Tyr	Ala	Leu	Lys	Val	Lys	Glu	Cys	Pro	Gln	Ile	Leu
			65					70					75		80

Phe	Leu	Arg	Gly	Asn	Arg	Ile	Leu	Tyr	Arg	Glu	Lys	Gly	Ser	Pro	Phe
							85							90	95

Leu

<210> 47

<211> 983

<212> DNA

<213> *Salsola komarovii*

<220>

<221> CDS

<222> (1)..(762)

<400> 47

atg ttc ctt cat cac cac ttt tca tct tca tct tct tct ttt ctt ctt 48

Met Phe Leu His His His Phe Ser Ser Ser Ser Ser Ser Phe Leu Leu

1 5 10 15

ctc ttc ttc tct ctc cta ata ttc ctt tca tct gct aat ctt tat cat 96

Leu Phe Phe Ser Leu Leu Ile Phe Leu Ser Ser Ala Asn Leu Tyr His

20 25 30

cag aat caa gga tct tgt agt gac ttt gaa tca gaa cca tca atg gct 144

Gln Asn Gln Gly Ser Cys Ser Asp Phe Glu Ser Glu Pro Ser Met Ala

35 40 45

act ctt ggt gga ttg cgc gaa tcc cat ggt gct tct aat gat gct gag 192

Thr Leu Gly Gly Leu Arg Glu Ser His Gly Ala Ser Asn Asp Ala Glu

50 55 60

att gaa acc ctt gct cgc ttt gct gtt gat gaa cac aac aaa aaa gag 240

Ile Glu Thr Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu

65 70 75 80

aat gca ttg ttg gag ttt gca agg gtt gta aag gca aag gaa cag gtg 288

Asn Ala Leu Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val	
85 90 95	
ggt gcg ggt aca ttg cat cac ttc act atc gaa gca att gaa gcg ggc	336
Val Ala Gly Thr Leu His His Phe Thr Ile Glu Ala Ile Glu Ala Gly	
100 105 110	
aag aag aag ctc tac gaa gcg aag gtg tgg gtg aag cca tgg atg aac	384
Lys Lys Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Met Asn	
115 120 125	
ttt aag gag ctg cag gaa ttt aag cat gct gat gaa tcc cct tca atc	432
Phe Lys Glu Leu Gln Glu Phe Lys His Ala Asp Glu Ser Pro Ser Ile	
130 135 140	
act cct tcc gac ctc ggc gct aat aga gaa ggg cat tct gga gga tgg	480
Thr Pro Ser Asp Leu Gly Ala Asn Arg Glu Gly His Ser Gly Gly Trp	
145 150 155 160	
aaa gat gtg cct gtc cat gac cct gaa gtg caa aat gca gca aat cat	528
Lys Asp Val Pro Val His Asp Pro Glu Val Gln Asn Ala Ala Asn His	
165 170 175	
gct ctt aag acc ttg caa caa aga tcc aac tcc tta ttt cct tat gaa	576
Ala Leu Lys Thr Leu Gln Gln Arg Ser Asn Ser Leu Phe Pro Tyr Glu	
180 185 190	
ctg cag gaa gtt gct cat gct agg gct gag gtt ctg gaa gac act gcg	624
Leu Gln Glu Val Ala His Ala Arg Ala Glu Val Leu Glu Asp Thr Ala	
195 200 205	
aag ttt aac ctg cac ctc aag gtg aag aga gga aac aag gat gag ttt	672
Lys Phe Asn Leu His Leu Lys Val Lys Arg Gly Asn Lys Asp Glu Phe	
210 215 220	
ttc aat gtg gag gtg cac aaa aac agc gaa gga aac tac aac ctt aat	720

Phe Asn Val Glu Val His Lys Asn Ser Glu Gly Asn Tyr Asn Leu Asn
 225 230 235 240

cag atg ggg aac gtt gag ccc gag gtt gag aaa agt agt gtt 762
 Gln Met Gly Asn Val Glu Pro Glu Val Glu Lys Ser Ser Val
 245 250

tagactcggt gaggtgttg taagtactcg ttcgtaactt ttctgatggt caggcaagta 822

tggagtaagg actagactac tagtactagt aagtacagct gacttggttt gagtaaaata 882

acctcgactt tggttgcacc atcatatctt gtatgtttat ggctttgtca atgtattgta 942

agtgaagatt gtttgcttga tctaaaaaaaa aaaaaaaaaa a 983

<210> 48

<211> 254

<212> PRT

<213> Salsola komarovii

<400> 48

Met Phe Leu His His His Phe Ser Ser Ser Ser Ser Ser Phe Leu Leu
 1 5 10 15

Leu Phe Phe Ser Leu Leu Ile Phe Leu Ser Ser Ala Asn Leu Tyr His
 20 25 30

Gln Asn Gln Gly Ser Cys Ser Asp Phe Glu Ser Glu Pro Ser Met Ala
 35 40 45

Thr Leu Gly Gly Leu Arg Glu Ser His Gly Ala Ser Asn Asp Ala Glu
 50 55 60

Ile Glu Thr Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu
 65 70 75 80

Asn Ala Leu Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val
85 90 95

Val Ala Gly Thr Leu His His Phe Thr Ile Glu Ala Ile Glu Ala Gly
100 105 110

Lys Lys Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Met Asn
115 120 125

Phe Lys Glu Leu Gln Glu Phe Lys His Ala Asp Glu Ser Pro Ser Ile
130 135 140

Thr Pro Ser Asp Leu Gly Ala Asn Arg Glu Gly His Ser Gly Gly Trp
145 150 155 160

Lys Asp Val Pro Val His Asp Pro Glu Val Gln Asn Ala Ala Asn His
165 170 175

Ala Leu Lys Thr Leu Gln Gln Arg Ser Asn Ser Leu Phe Pro Tyr Glu
180 185 190

Leu Gln Glu Val Ala His Ala Arg Ala Glu Val Leu Glu Asp Thr Ala
195 200 205

Lys Phe Asn Leu His Leu Lys Val Lys Arg Gly Asn Lys Asp Glu Phe
210 215 220

Phe Asn Val Glu Val His Lys Asn Ser Glu Gly Asn Tyr Asn Leu Asn
225 230 235 240

Gln Met Gly Asn Val Glu Pro Glu Val Glu Lys Ser Ser Val
245 250

<210> 49

<211> 543

<212> DNA

<213> *Salsola komarovii*

<220>

<221> CDS

<222> (3)..(389)

<400> 49

aa aat aag gtt gac tta gct cga gat ttc acc ttc ata gac gac gtc 47

Asn Lys Val Asp Leu Ala Arg Asp Phe Thr Phe Ile Asp Asp Val

1 5 10 15

gta aag ggg tgc tta ggt tca ctg gat tct tcc ggt aag agt acc ggt 95

Val Lys Gly Cys Leu Gly Ser Leu Asp Ser Ser Gly Lys Ser Thr Gly

20 25 30

agc ggc ggt aaa aaa cgt ggg ccc gct ccg tac aga atc tac aac ttg 143

Ser Gly Gly Lys Lys Arg Gly Pro Ala Pro Tyr Arg Ile Tyr Asn Leu

35 40 45

ggg aac act caa ccg gtc act gta ccg aca ctt gtc ggt atc cta gag 191

Gly Asn Thr Gln Pro Val Thr Val Pro Thr Leu Val Gly Ile Leu Glu

50 55 60

aag cat ctc aaa gtt aag gcc aag aag aat gtg gtt gag atg ccc gga 239

Lys His Leu Lys Val Lys Ala Lys Lys Asn Val Val Glu Met Pro Gly

65 70 75

aat ggt gac gtg ccc ttc aca cat gcg aat atc tct ttg gcc cga aaa 287

Asn Gly Asp Val Pro Phe Thr His Ala Asn Ile Ser Leu Ala Arg Lys

80 85 90 95

gat ttc ggg tat aaa ccc act acc gat ttg caa acc ggg ttg aaa aag 335

Asp Phe Gly Tyr Lys Pro Thr Thr Asp Leu Gln Thr Gly Leu Lys Lys

	85	90	95
Phe Gly Tyr Lys Pro Thr Thr Asp Leu Gln Thr Gly Leu Lys Lys Phe			
	100	105	110
Val Arg Trp Tyr Leu Thr Tyr Tyr Gly Tyr Asn Asn Gly Lys Pro Val			
	115	120	125

Asn

<210> 51
 <211> 1219
 <212> DNA
 <213> Sueada japonica

<220>
 <221> CDS
 <222> (2).. (871)

<400> 51
 c aca gga gca aac aaa gga ata gga ctt gaa cta tgc aaa caa cta gct 49
 Thr Gly Ala Asn Lys Gly Ile Gly Leu Glu Leu Cys Lys Gln Leu Ala
 1 5 10 15

gct aaa gga gtt gta gta gtt ctc act tct aga gat gga aaa aga ggc 97
 Ala Lys Gly Val Val Val Val Leu Thr Ser Arg Asp Gly Lys Arg Gly
 20 25 30

tta caa gct cat gaa aat ctc att aaa tct gga att aat cct gaa aat 145
 Leu Gln Ala His Glu Asn Leu Ile Lys Ser Gly Ile Asn Pro Glu Asn
 35 40 45

ctt cac ttt cat cag ctc gat gtt act gac atc act agt att gct gct 193

Met	Leu	Arg	Asp	Phe	Lys	Asp	Cys	Ser	Phe	Lys	Glu	Lys	Gly	Trp	Pro	
195				200				205								
.																
aaa	aat	ctg	gca	gcc	tat	ata	gtt	tca	aag	gcg	gcc	ttg	agt	gca	tac	673
Lys	Asn	Leu	Ala	Ala	Tyr	Ile	Val	Ser	Lys	Ala	Ala	Leu	Ser	Ala	Tyr	
210				215				220								
aca	aga	ata	ctg	gct	aag	aaa	tac	cca	tca	atc	atg	atc	aac	tgt	att	721
Thr	Arg	Ile	Leu	Ala	Lys	Lys	Tyr	Pro	Ser	Ile	Met	Ile	Asn	Cys	Ile	
225				230				235				240				
tgc	cct	ggc	ttt	gtc	aaa	act	gac	atc	aat	gga	aac	aca	gga	cac	ttg	769
Cys	Pro	Gly	Phe	Val	Lys	Thr	Asp	Ile	Asn	Gly	Asn	Thr	Gly	His	Leu	
245				250				255								
ccg	gtt	gaa	gaa	ggg	gca	gcg	agt	ctg	gca	agg	tta	gcg	ttg	atg	ccc	817
Pro	Val	Glu	Glu	Gly	Ala	Ala	Ser	Leu	Ala	Arg	Leu	Ala	Leu	Met	Pro	
260				265				270								
caa	att	tta	cct	tct	gga	cta	ttc	ttt	cag	aga	act	gaa	gtt	tct	tcg	865
Gln	Ile	Leu	Pro	Ser	Gly	Leu	Phe	Phe	Gln	Arg	Thr	Glu	Val	Ser	Ser	
275				280				285								
ttt	gaa	taaaacaatt	tgctatttca	aaccaacacc	acatatctat	gaagtttcca										921
Phe	Glu															
290																
ttt	gttaggca	tcttttacgaa	aaaaataaga	catctgcaat	actgttactg	gaaaatgcaa										981
-	-	-	-	-	-	-										
gt	tacttttt	tcatgtatgc	atggcgagct	tattttattct	gactgcaaca	ataagattct										1041
gtt	cttttcaa	ggcactctaa	ggaatgctga	tgtaccgttc	tcaaacaagc	agacaagtag										1101
acac	gtttga	ttgtcatgtc	ttcattcgta	caatcathtt	gtgtttgtat	gttgagcatg										1161
ttta	actaat	tacaagagtg	taattaagat	caacttttat	aaaaaaaaaa	aaaaaaaaaa										1219

<210> 52

<211> 290

<212> PRT

<213> Sueada japonica

<400> 52

Thr Gly Ala Asn Lys Gly Ile Gly Leu Glu Leu Cys Lys Gln Leu Ala
1 5 10 15

Ala Lys Gly Val Val Val Val Leu Thr Ser Arg Asp Gly Lys Arg Gly
20 25 30

Leu Gln Ala His Glu Asn Leu Ile Lys Ser Gly Ile Asn Pro Glu Asn
35 40 45

Leu His Phe His Gln Leu Asp Val Thr Asp Ile Thr Ser Ile Ala Ala
50 55 60

Ile Ala Gly Phe Ile Asn Ser Lys Phe Gly Lys Leu Asp Ile Leu Val
65 70 75 80

Asn Asn Ala Gly Ile Ile Gly Asp Met Val Asn Phe Asp Ala Leu Ile
85 90 95

Ala Ala Gly Phe Gly Thr Pro Arg Glu Gln Ile Asn Leu Glu Asp Ser
100 105 110

Pro Gly Thr Val Thr Gln Thr Tyr Glu Leu Thr Lys Glu Cys Leu Gln
115 120 125

Thr Asn Tyr Tyr Gly Ala Lys Arg Thr Val Glu Ala Leu Leu Pro Leu
130 135 140

Leu Lys Leu Ser Asp Ser Pro Arg Ile Val Asn Val Ser Ser Phe Leu

145	150	155	160
Gly Arg Leu Thr Tyr Ile Pro Asn Glu Thr Ile Arg Gly Val Leu Arg			
165	170	175	
Asp Ala Glu Ser Leu Thr Glu Glu Arg Ile Asp Glu Ile Leu Asn Asp			
180	185	190	
Met Leu Arg Asp Phe Lys Asp Cys Ser Phe Lys Glu Lys Gly Trp Pro			
195	200	205	
Lys Asn Leu Ala Ala Tyr Ile Val Ser Lys Ala Ala Leu Ser Ala Tyr			
210	215	220	
Thr Arg Ile Leu Ala Lys Lys Tyr Pro Ser Ile Met Ile Asn Cys Ile			
225	230	235	240
Cys Pro Gly Phe Val Lys Thr Asp Ile Asn Gly Asn Thr Gly His Leu			
245	250	255	
Pro Val Glu Glu Gly Ala Ala Ser Leu Ala Arg Leu Ala Leu Met Pro			
260	265	270	
Gln Ile Leu Pro Ser Gly Leu Phe Phe Gln Arg Thr Glu Val Ser Ser			
275	280	285	
Phe Glu			
290			

<210> 53

<211> 1148

<212> DNA

<213> Sueada japonica

<220>

<221> CDS

<222> (3)..(848)

<400> 53

ga agc agg ccg gat atc cat gtt gaa caa gct cat tca gat gat att 47

Ser Arg Pro Asp Ile His Val Glu Gln Ala His Ser Asp Asp Ile

1 5 10 15

act ggg ttg aaa ttc tca tgt gat ggt cgt cat ctg ttg tct aga agt 95

Thr Gly Leu Lys Phe Ser Cys Asp Gly Arg His Leu Leu Ser Arg Ser

20 25 30

ttt gat tgc aca ctt aag gtt tgg gac ttg cgc caa atg aag cgg tct 143

Phe Asp Cys Thr Leu Lys Val Trp Asp Leu Arg Gln Met Lys Arg Ser

35 40 45

ctt aag gtg ttt gat gaa tta cca aat cac tat gct caa acg aat gtc 191

Leu Lys Val Phe Asp Glu Leu Pro Asn His Tyr Ala Gln Thr Asn Val

50 55 60

tca ttt agt cca gat gag cag ctc atc ttg act ggt aca tct gta gaa 239

Ser Phe Ser Pro Asp Glu Gln Leu Ile Leu Thr Gly Thr Ser Val Glu

65 70 75

agg gat agc cca act gga gga ttg ttg tgc ttt tat gat cgg gaa aaa 287

Arg Asp Ser Pro Thr Gly Gly Leu Leu Cys Phe Tyr Asp Arg Glu Lys

80 85 90 95

ctt gaa cta gta tca aaa gtt ggc att tct cct act tgc agt gtt gtg 335

Leu Glu Leu Val Ser Lys Val Gly Ile Ser Pro Thr Cys Ser Val Val

100 105 110

caa tgt gcc tgg cac cca agg ctg aat cag gtt ttt gcc act gct gga 383

Gln Cys Ala Trp His Pro Arg Leu Asn Gln Val Phe Ala Thr Ala Gly

115 120 125

aat aaa agc caa gga ggt aca cat gta ctc tat gat cca acc atg agt	431
Asn Lys Ser Gln Gly Gly Thr His Val Leu Tyr Asp Pro Thr Met Ser	
130 135 140	
gag aga ggt gct ctt gtg tgt gtt gct cgt gca cca agg atg aaa tca	479
Glu Arg Gly Ala Leu Val Cys Val Ala Arg Ala Pro Arg Met Lys Ser	
145 150 155	
gtg gat gat ttt gag gtg cag ccg gtt ata cat aac cct cac gca ctt	527
Val Asp Asp Phe Glu Val Gln Pro Val Ile His Asn Pro His Ala Leu	
160 165 170 175	
ccc ttg ttc aga gat cag cca agc cgc aaa cgt caa aga gag aag att	575
Pro Leu Phe Arg Asp Gln Pro Ser Arg Lys Arg Gln Arg Glu Lys Ile	
180 185 190	
ctg aag gac cca ata aaa tcc cac aaa cca gag ctt cct atg tca gga	623
Leu Lys Asp Pro Ile Lys Ser His Lys Pro Glu Leu Pro Met Ser Gly	
195 200 205	
cct ggc cat ggt ggc aga act ggt aca tca tcg ggt agt ttg tta aca	671
Pro Gly His Gly Gly Arg Thr Gly Thr Ser Ser Gly Ser Leu Leu Thr	
210 215 220	
caa tat ctc ctc aag caa ggg ggc atg ttg aaa gag aca tgg atg gat	719
Gln Tyr Leu Leu Lys Gln Gly Gly Met Leu Lys Glu Thr Trp Met Asp	
225 230 235	
gaa gat ccc aga gaa gct att ctc aag tat gct gat gct gca gaa aag	767
Glu Asp Pro Arg Glu Ala Ile Leu Lys Tyr Ala Asp Ala Ala Glu Lys	
240 245 250 255	
gat cca aag ttt att gcc ccg gct tat gct gag act cag ccc aag cca	815
Asp Pro Lys Phe Ile Ala Pro Ala Tyr Ala Glu Thr Gln Pro Lys Pro	
260 265 270	

gtc ttt gag gat tct gat aag gaa gat gaa gaa taattcatct ttgcagtg 868
Val Phe Glu Asp Ser Asp Lys Glu Asp Glu Glu

275 280

ttggattaat ttaatttgag aatattatac tgtgtatatt aatagccaat tttcaggcg 928

aatgatatgc ttctcacatt acatgctgag ttttatttgc tgctacagat ttagatgaa 988

taggttaatg taaacacaag catagagatt agaatataga aatgattctg tatccaaaac 1048

acaatttiat caccagatgg tatcaaaagc tgtattgact gttgagtaat gtcattaacc 1108

actttcactc cccaaaaaaa aaaaaaaaaa aaaaaaaaaa 1148

<210> 54

<211> 282

<212> PRT

<213> Sueada japonica

<400> 54

Ser Arg Pro Asp Ile His Val Glu Gln Ala His Ser Asp Asp Ile Thr

1 5 10 15

Gly Leu Lys Phe Ser Cys Asp Gly Arg His Leu Leu Ser Arg Ser Phe

20 25 30

Asp Cys Thr Leu Lys Val Trp Asp Leu Arg Gln Met Lys Arg Ser Leu

35 40 45

Lys Val Phe Asp Glu Leu Pro Asn His Tyr Ala Gln Thr Asn Val Ser

50 55 60

Phe Ser Pro Asp Glu Gln Leu Ile Leu Thr Gly Thr Ser Val Glu Arg

65 70 75 80

Asp Ser Pro Thr Gly Gly Leu Leu Cys Phe Tyr Asp Arg Glu Lys Leu
85 90 95

Glu Leu Val Ser Lys Val Gly Ile Ser Pro Thr Cys Ser Val Val Gln
100 105 110

Cys Ala Trp His Pro Arg Leu Asn Gln Val Phe Ala Thr Ala Gly Asn
115 120 125

Lys Ser Gln Gly Gly Thr His Val Leu Tyr Asp Pro Thr Met Ser Glu
130 135 140

Arg Gly Ala Leu Val Cys Val Ala Arg Ala Pro Arg Met Lys Ser Val
145 150 155 160

Asp Asp Phe Glu Val Gln Pro Val Ile His Asn Pro His Ala Leu Pro
165 170 175

Leu Phe Arg Asp Gln Pro Ser Arg Lys Arg Gln Arg Glu Lys Ile Leu
180 185 190

Lys Asp Pro Ile Lys Ser His Lys Pro Glu Leu Pro Met Ser Gly Pro
195 200 205

Gly His Gly Gly Arg Thr Gly Thr Ser Ser Gly Ser Leu Leu Thr Gln
210 215 220

Tyr Leu Leu Lys Gln Gly Gly Met Leu Lys Glu Thr Trp Met Asp Glu
225 230 235 240

Asp Pro Arg Glu Ala Ile Leu Lys Tyr Ala Asp Ala Ala Glu Lys Asp
245 250 255

Pro Lys Phe Ile Ala Pro Ala Tyr Ala Glu Thr Gln Pro Lys Pro Val
260 265 270

Phe Glu Asp Ser Asp Lys Glu Asp Glu Glu
 275 280

<210> 55

<211> 1193

<212> DNA

<213> Avicennia marina

<220>

<221> CDS

<222> (3)..(815)

<400> 55

gt gca cct gag tta ctt ctt gga gca aag cat tat aca agt gct gtt 47

Ala Pro Glu Leu Leu Leu Gly Ala Lys His Tyr Thr Ser Ala Val

1 5 10 15

gac atg tgg gct gtg ggc tgc att ttt gct gag ctt ctg act cta aag 95

Asp Met Trp Ala Val Gly Cys Ile Phe Ala Glu Leu Leu Thr Leu Lys

20 25 30

cca cta ttt caa ggg caa gaa gta aaa ggg act tct aat cca ttt cag 143

Pro Leu Phe Gln Gly Gln Glu Val Lys Gly Thr Ser Asn Pro Phe Gln

35 40 45

ctt gat caa ctt gac aaa atc ttt aag gtc cta ggt cat ccc acg caa 191

Leu Asp Gln Leu Asp Lys Ile Phe Lys Val Leu Gly His Pro Thr Gln

50 55 60

gaa aag tgg ccc aca cta gcg aat ctt cca cat tgg cag tct gat gtg 239

Glu Lys Trp Pro Thr Leu Ala Asn Leu Pro His Trp Gln Ser Asp Val

65 70 75

caa cgt atc caa ggg ctc aaa tac gac aat act gga ctt tac aat gtt 287
 Gln Arg Ile Gln Gly Leu Lys Tyr Asp Asn Thr Gly Leu Tyr Asn Val
 80 85 90 95

gtt cat ctc tcc ccc aaa aat cca gca tat gac ctt ctc tca aag atg 335
 Val His Leu Ser Pro Lys Asn Pro Ala Tyr Asp Leu Leu Ser Lys Met
 100 105 110

ctt gag tat gat cct aga aaa aga ata aca gct aca caa gct ctt gag 383
 Leu Glu Tyr Asp Pro Arg Lys Arg Ile Thr Ala Thr Gln Ala Leu Glu
 115 120 125

cat gag tat ttt cgc atg gaa cct ttg ccg gga cgc aac gct ctg gta 431
 His Glu Tyr Phe Arg Met Glu Pro Leu Pro Gly Arg Asn Ala Leu Val
 130 135 140

cca cca cag cct ggg gag aaa att gtg aac tac cca aca cga cca gtg 479
 Pro Pro Gln Pro Gly Glu Lys Ile Val Asn Tyr Pro Thr Arg Pro Val
 145 150 155

gac aca aat act gat att gaa gga aca atc agc ctc cag ccc tct caa 527
 Asp Thr Asn Thr Asp Ile Glu Gly Thr Ile Ser Leu Gln Pro Ser Gln
 160 165 170 175

ccg gta tca tct ggg aat tct gtg tct ggg gcc cta gcc ggt cct cat 575
 Pro Val Ser Ser Gly Asn Ser Val Ser Gly Ala Leu Ala Gly Pro His
 180 185 190

gta atg caa aat aga tcc atg cct cgg cca atg ccc atg gtt ggc gtg 623
 Val Met Gln Asn Arg Ser Met Pro Arg Pro Met Pro Met Val Gly Val
 195 200 205

caa cgc atg caa cct cca ggg atc cca cac tat ggt ctt gct tct cag 671
 Gln Arg Met Gln Pro Pro Gly Ile Pro His Tyr Gly Leu Ala Ser Gln
 210 215 220

gca gga atg ggt gga gta aat cct ggt ggc atc cca att cag cgg gga 719
 Ala Gly Met Gly Gly Val Asn Pro Gly Gly Ile Pro Ile Gln Arg Gly
 225 230 235

gtt cct gct cag gct cat caa cag cag cag atg aga agg aaa gac cct 767
 Val Pro Ala Gln Ala His Gln Gln Gln Gln Met Arg Arg Lys Asp Pro
 240 245 250 255

gga atg ggg atg act gga tat cct cca caa cag aaa tca agg cgc ttt 815
 Gly Met Gly Met Thr Gly Tyr Pro Pro Gln Gln Lys Ser Arg Arg Phe
 260 265 270

tgagagtccg ggtggatttg gagcctaagt gggaggacaa atacacattc caatcaaatt 875

agaggaaacc ttaaattaat cttccagtca gctgaaacga caccagtga accaaatgat 935

ctgaccccat ttccaggatt gcatgtatit attaggagga atacacgaat gaagattcga 995

gtctagtgcc aaattattct aacatacctt catcatttgt tcctactaca ttccgacgtt 1055

atatgtttca actagtggaa gggttttctgc agtccaccca tgtggcacia acatgattca 1115

tagcatgcca agcaacactt tactggtgtg taccaaggca atttctctat ttccaagcca 1175

aaaaaaaaa aaaaaaaaa 1193

<210> 56

<211> 271

<212> PRT

<213> Avicennia marina

<400> 56

Ala Pro Glu Leu Leu Leu Gly Ala Lys His Tyr Thr Ser Ala Val Asp
 1 5 10 15

Met Trp Ala Val Gly Cys Ile Phe Ala Glu Leu Leu Thr Leu Lys Pro
20 25 30

Leu Phe Gln Gly Gln Glu Val Lys Gly Thr Ser Asn Pro Phe Gln Leu
35 40 45

Asp Gln Leu Asp Lys Ile Phe Lys Val Leu Gly His Pro Thr Gln Glu
50 55 60

Lys Trp Pro Thr Leu Ala Asn Leu Pro His Trp Gln Ser Asp Val Gln
65 70 75 80

Arg Ile Gln Gly Leu Lys Tyr Asp Asn Thr Gly Leu Tyr Asn Val Val
85 90 95

His Leu Ser Pro Lys Asn Pro Ala Tyr Asp Leu Leu Ser Lys Met Leu
100 105 110

Glu Tyr Asp Pro Arg Lys Arg Ile Thr Ala Thr Gln Ala Leu Glu His
115 120 125

Glu Tyr Phe Arg Met Glu Pro Leu Pro Gly Arg Asn Ala Leu Val Pro
130 135 140

Pro Gln Pro Gly Glu Lys Ile Val Asn Tyr Pro Thr Arg Pro Val Asp
145 150 155 160

Thr Asn Thr Asp Ile Glu Gly Thr Ile Ser Leu Gln Pro Ser Gln Pro
165 170 175

Val Ser Ser Gly Asn Ser Val Ser Gly Ala Leu Ala Gly Pro His Val
180 185 190

Met Gln Asn Arg Ser Met Pro Arg Pro Met Pro Met Val Gly Val Gln
195 200 205

Arg Met Gln Pro Pro Gly Ile Pro His Tyr Gly Leu Ala Ser Gln Ala
 210 215 220

Gly Met Gly Gly Val Asn Pro Gly Gly Ile Pro Ile Gln Arg Gly Val
 225 230 235 240

Pro Ala Gln Ala His Gln Gln Gln Gln Met Arg Arg Lys Asp Pro Gly
 245 250 255

Met Gly Met Thr Gly Tyr Pro Pro Gln Gln Lys Ser Arg Arg Phe
 260 265 270

<210> 57

<211> 1195

<212> DNA

<213> Sueada japonica

<220>

<221> CDS

<222> (116).. (1195)

<400> 57

gcaaaagtaa gagtgaaaga acacaaacca actttctatt ttcagctcaa atcaaattca 60

atagtggcaa aacaatagag ggcaaattct cattgcccaa ttcaaatttg gtaaa atg 118

Met

1

gct caa aag cat ttg aaa gaa ctt ctc aaa gaa gat caa gaa ccc ttt 166

Ala Gln Lys His Leu Lys Glu Leu Leu Lys Glu Asp Gln Glu Pro Phe

5

10

15

cat tta aag gat tac att gca act aaa aaa tgt caa ctt ttg aag aag 214

His Leu Lys Asp Tyr Ile Ala Thr Lys Lys Cys Gln Leu Leu Lys Lys

20	25	30	
caa gaa tta gta gta ccc aaa tca aaa ctt caa ctc aaa aag cca aag			262
Gln Glu Leu Val Val Pro Lys Ser Lys Leu Gln Leu Lys Lys Pro Lys			
35	40	45	
cca aaa cca att tca aaa agc act tca gtt ttg tgc aaa aat gct tgc			310
Pro Lys Pro Ile Ser Lys Ser Thr Ser Val Leu Cys Lys Asn Ala Cys			
50	55	60	65
ttt tta tct tta caa gaa tcc cct gac ctc aga aaa tcc ccc aaa cta			358
Phe Leu Ser Leu Gln Glu Ser Pro Asp Leu Arg Lys Ser Pro Lys Leu			
70	75	80	
ttt gat ttt cca cct tcc cct gtt tct aac aaa agc cca aac aga gta			406
Phe Asp Phe Pro Pro Ser Pro Val Ser Asn Lys Ser Pro Asn Arg Val			
85	90	95	
ttc ctc aat gtt cct gct aaa act gct gct ctt ctt ctt gaa gct gct			454
Phe Leu Asn Val Pro Ala Lys Thr Ala Ala Leu Leu Leu Glu Ala Ala			
100	105	110	
att cga att caa acc cac aaa tct aaa ccc aaa acc cag att aaa aat			502
Ile Arg Ile Gln Thr His Lys Ser Lys Pro Lys Thr Gln Ile Lys Asn			
115	120	125	
tgc ggt ttt ggg cta ttc ggg tca atg tta aag cga tta aat ctt cga			550
Ser Gly Phe Gly Leu Phe Gly Ser Met Leu Lys Arg Leu Asn Leu Arg			
130	135	140	145
aat cgt acc caa aaa atc aag tca aaa aca gag gaa caa aac aga gga			598
Asn Arg Thr Gln Lys Ile Lys Ser Lys Thr Glu Glu Gln Asn Arg Gly			
150	155	160	
tgc tct gtt ttg agg agt gtt gaa gaa gaa aaa act acc acc att tct			646
Cys Ser Val Leu Arg Ser Val Glu Glu Glu Lys Thr Thr Thr Ile Ser			

165	170	175	
tct tct tca tct tca tct tct tca aca tca tcg tat tct tcg tgt tct	694		
Ser Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Tyr Ser Ser Cys Ser			
180	185	190	
tgc aat gag agg tta agt agt ttg gat ttg gag agt tct agc agt gga	742		
Cys Asn Glu Arg Leu Ser Ser Leu Asp Leu Glu Ser Ser Ser Ser Gly			
195	200	205	
aga tca tta cat gat gaa gat gaa gat gaa gat gaa gat gat gaa ttt	790		
Arg Ser Leu His Asp Glu Asp Glu Asp Glu Asp Glu Asp Asp Glu Phe			
210	215	220	225
gag ttt aca aat gtt tta aga gaa aat aat aat gat gat aaa aat gga	838		
Glu Phe Thr Asn Val Leu Arg Glu Asn Asn Asn Asp Asp Lys Asn Gly			
230	235	240	
ggt tat tat tca gga att tgc tta agt cct ttg agt cca ttt cgt ttt	886		
Gly Tyr Tyr Ser Gly Ile Cys Leu Ser Pro Leu Ser Pro Phe Arg Phe			
245	250	255	
gct ctt cat aaa aac tct tct cct gaa cgt tgc tct cct gct aaa tcc	934		
Ala Leu His Lys Asn Ser Ser Pro Glu Arg Cys Ser Pro Ala Lys Ser			
260	265	270	
cct gtt cgt tgc aaa ttt gag ggt aat gct aaa tat gaa caa gaa agc	982		
Pro Val Arg Cys Lys Phe Glu Gly Asn Ala Lys Tyr Glu Gln Glu Ser			
275	280	285	
tta ata aag ttt gaa gac gaa gat gaa gaa gac aaa gag caa aat agc	1030		
Leu Ile Lys Phe Glu Asp Glu Asp Glu Glu Asp Lys Glu Gln Asn Ser			
290	295	300	305
cct gtt tcc gtg ctc gat cct cca ttc gag gat gat tac gat ggg cat	1078		
Pro Val Ser Val Leu Asp Pro Pro Phe Glu Asp Asp Tyr Asp Gly His			

310	315	320	
gag gag gat agc tac gag gac atc gaa tgc agc tat gct ttt gta caa			1126
Glu Glu Asp Ser Tyr Glu Asp Ile Glu Cys Ser Tyr Ala Phe Val Gln			
325	330	335	

aga gca caa caa gag tta ttg cac aga ctt cac cgg ttc cag aag cta			1174
Arg Ala Gln Gln Glu Leu Leu His Arg Leu His Arg Phe Gln Lys Leu			
340	345	350	

gcg gag ttg gac cca att gaa			1195
Ala Glu Leu Asp Pro Ile Glu			
355	360		

<210> 58

<211> 360

<212> PRT

<213> Sueada japonica

<400> 58

Met Ala Gln Lys His Leu Lys Glu Leu Leu Lys Glu Asp Gln Glu Pro			
1	5	10	15

Phe His Leu Lys Asp Tyr Ile Ala Thr Lys Lys Cys Gln Leu Leu Lys			
20	25	30	

Lys Gln Glu Leu Val Val Pro Lys Ser Lys Leu Gln Leu Lys Lys Pro			
35	40	45	

Lys Pro Lys Pro Ile Ser Lys Ser Thr Ser Val Leu Cys Lys Asn Ala			
50	55	60	

Cys Phe Leu Ser Leu Gln Glu Ser Pro Asp Leu Arg Lys Ser Pro Lys			
65	70	75	80

Leu Phe Asp Phe Pro Pro Ser Pro Val Ser Asn Lys Ser Pro Asn Arg
85 90 95

Val Phe Leu Asn Val Pro Ala Lys Thr Ala Ala Leu Leu Leu Glu Ala
100 105 110

Ala Ile Arg Ile Gln Thr His Lys Ser Lys Pro Lys Thr Gln Ile Lys
115 120 125

Asn Ser Gly Phe Gly Leu Phe Gly Ser Met Leu Lys Arg Leu Asn Leu
130 135 140

Arg Asn Arg Thr Gln Lys Ile Lys Ser Lys Thr Glu Glu Gln Asn Arg
145 150 155 160

Gly Cys Ser Val Leu Arg Ser Val Glu Glu Glu Lys Thr Thr Thr Ile
165 170 175

Ser Ser Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Tyr Ser Ser Cys
180 185 190

Ser Cys Asn Glu Arg Leu Ser Ser Leu Asp Leu Glu Ser Ser Ser Ser
195 200 205

Gly Arg Ser Leu His Asp Glu Asp Glu Asp Glu Asp Glu Asp Asp Glu
210 215 220

Phe Glu Phe Thr Asn Val Leu Arg Glu Asn Asn Asn Asp Asp Lys Asn
225 230 235 240

Gly Gly Tyr Tyr Ser Gly Ile Cys Leu Ser Pro Leu Ser Pro Phe Arg
245 250 255

Phe Ala Leu His Lys Asn Ser Ser Pro Glu Arg Cys Ser Pro Ala Lys
260 265 270

Ser Pro Val Arg Cys Lys Phe Glu Gly Asn Ala Lys Tyr Glu Gln Glu
 275 280 285

Ser Leu Ile Lys Phe Glu Asp Glu Asp Glu Glu Asp Lys Glu Gln Asn
 290 295 300

Ser Pro Val Ser Val Leu Asp Pro Pro Phe Glu Asp Asp Tyr Asp Gly
 305 310 315 320

His Glu Glu Asp Ser Tyr Glu Asp Ile Glu Cys Ser Tyr Ala Phe Val
 325 330 335

Gln Arg Ala Gln Gln Glu Leu Leu His Arg Leu His Arg Phe Gln Lys
 340 345 350

Leu Ala Glu Leu Asp Pro Ile Glu
 355 360

<210> 59

<211> 1301

<212> DNA

<213> *Salsola komarovii*

<220>

<221> CDS

<222> (3).. (815)

<400> 59

gt gag gtt gac gat agc gtt aat agt cta cag gca gat gtt gac aac 47
 Glu Val Asp Asp Ser Val Asn Ser Leu Gln Ala Asp Val Asp Asn
 1 5 10 15

ctt tca att gag gaa cgc aga ttg gat gaa cag ata agg gaa atg caa 95
 Leu Ser Ile Glu Glu Arg Arg Leu Asp Glu Gln Ile Arg Glu Met Gln

20	25	30	
gaa aga ttg agg gaa atg agt gaa gat gat atc aat cag aag tgg ctt			143
Glu Arg Leu Arg Glu Met Ser Glu Asp Asp Ile Asn Gln Lys Trp Leu			
35	40	45	
ttt gta act gaa gaa gac ata aag ggt tta cct tgt ttt cag aat gaa			191
Phe Val Thr Glu Glu Asp Ile Lys Gly Leu Pro Cys Phe Gln Asn Glu			
50	55	60	
acc tta att gca att aaa gct cca cat gga aca act ttg gag gtt cca			239
Thr Leu Ile Ala Ile Lys Ala Pro His Gly Thr Thr Leu Glu Val Pro			
65	70	75	
gat cca gat gag gct gtc gat tat cct caa aga aga tac aag ata gtt			287
Asp Pro Asp Glu Ala Val Asp Tyr Pro Gln Arg Arg Tyr Lys Ile Val			
80	85	90	95
ctt agg agc aca atg ggt cct att gat gta tat tta gtc agt caa ttt			335
Leu Arg Ser Thr Met Gly Pro Ile Asp Val Tyr Leu Val Ser Gln Phe			
100	105	110	
gaa gag aag ttt gag gag atc agt ggt gct gac ggt cca cta agt ata			383
Glu Glu Lys Phe Glu Glu Ile Ser Gly Ala Asp Gly Pro Leu Ser Ile			
115	120	125	
cca agt acc tca ggt gat gac aaa cac aca act gtt gca gct aag gaa			431
Pro Ser Thr Ser Gly Asp Asp Lys His Thr Thr Val Ala Ala Lys Glu			
130	135	140	
gaa agc aat ggc aat gag att gaa ata gaa gga caa ggg acc cat aga			479
Glu Ser Asn Gly Asn Glu Ile Glu Ile Glu Gly Gln Gly Thr His Arg			
145	150	155	
atc tgc tca gat tcc aac gct cag caa gac ttt gtg agt gga att atg			527
Ile Cys Ser Asp Ser Asn Ala Gln Gln Asp Phe Val Ser Gly Ile Met			

160	165	170	175	
aag ata gtg cct gaa gtt gat agt gat gca gat tac tgg ttg cta tcg				575
Lys Ile Val Pro Glu Val Asp Ser Asp Ala Asp Tyr Trp Leu Leu Ser				
	180	185	190	
gat gct gat gtt agc att act gac atg tgg gga act gat tct gga gtt				623
Asp Ala Asp Val Ser Ile Thr Asp Met Trp Gly Thr Asp Ser Gly Val				
	195	200	205	
gaa tgg aat gaa tta ggg act ata cat gaa gac tat gcc gtg gct aat				671
Glu Trp Asn Glu Leu Gly Thr Ile His Glu Asp Tyr Ala Val Ala Asn				
	210	215	220	
gtt ggc act tca cag cca caa agt cca cca aca agt gca aca gaa gtg				719
Val Gly Thr Ser Gln Pro Gln Ser Pro Pro Thr Ser Ala Thr Glu Val				
	225	230	235	
ctt cca gct aac atg aca agc agg aga ttg aca tgg agt ttt gag aga				767
Leu Pro Ala Asn Met Thr Ser Arg Arg Leu Thr Trp Ser Phe Glu Arg				
240	245	250	255	
att gcc aar att cat tca aat ggt cac tat tgc ttg gaa gtg agg etc				815
Ile Ala Lys Ile His Ser Asn Gly His Tyr Cys Leu Glu Val Arg Leu				
	260	265	270	
taactttcta ttattcatcc tgggatttgg gtacgaaagt ctgccttgaa gatgctgtaa				875
catgttgtgt attacaactg tgtgaatcta gtaagttggt agggtgagat tgttcctgat				935
cttattgcac agccggttgg gagagattga tcgctcaaca actgacaaaa ttggggcatg				995
ttaacggata gtatgcagtt gtaattttgt acatcacatt tgttgatttt agtcagtaca				1055
tcataactag ctcttcctat acttcttcaa ttgtcaactg gaatagattt ttagattaat				1115

tagatctctc ttgtatgga aatgtttcag ggtaacaagc cagaaattaa aatggtttta 1175

tgtgtaaaaa tatatactta aattgtttgt aggaagtttc tgatgggttg ttggatggct 1235

tttaacaact acatcgata aggaaattcg tatcacaat tcacaatgaa aaaaaaaaaa 1295

aaaaaa 1301

<210> 60

<211> 271

<212> PRT

<213> Salsola komarovii

<400> 60

Glu	Val	Asp	Asp	Ser	Val	Asn	Ser	Leu	Gln	Ala	Asp	Val	Asp	Asn	Leu
1				5					10					15	

Ser	Ile	Glu	Glu	Arg	Arg	Leu	Asp	Glu	Gln	Ile	Arg	Glu	Met	Gln	Glu
			20					25					30		

Arg	Leu	Arg	Glu	Met	Ser	Glu	Asp	Asp	Ile	Asn	Gln	Lys	Trp	Leu	Phe
			35					40					45		

Val	Thr	Glu	Glu	Asp	Ile	Lys	Gly	Leu	Pro	Cys	Phe	Gln	Asn	Glu	Thr
	50						55						60		

Leu	Ile	Ala	Ile	Lys	Ala	Pro	His	Gly	Thr	Thr	Leu	Glu	Val	Pro	Asp
65					70					75				80	

Pro	Asp	Glu	Ala	Val	Asp	Tyr	Pro	Gln	Arg	Arg	Tyr	Lys	Ile	Val	Leu
					85				90					95	

Arg	Ser	Thr	Met	Gly	Pro	Ile	Asp	Val	Tyr	Leu	Val	Ser	Gln	Phe	Glu
			100					105					110		

Glu Lys Phe Glu Glu Ile Ser Gly Ala Asp Gly Pro Leu Ser Ile Pro
115 120 125

Ser Thr Ser Gly Asp Asp Lys His Thr Thr Val Ala Ala Lys Glu Glu
130 135 140

Ser Asn Gly Asn Glu Ile Glu Ile Glu Gly Gln Gly Thr His Arg Ile
145 150 155 160

Cys Ser Asp Ser Asn Ala Gln Gln Asp Phe Val Ser Gly Ile Met Lys
165 170 175

Ile Val Pro Glu Val Asp Ser Asp Ala Asp Tyr Trp Leu Leu Ser Asp
180 185 190

Ala Asp Val Ser Ile Thr Asp Met Trp Gly Thr Asp Ser Gly Val Glu
195 200 205

Trp Asn Glu Leu Gly Thr Ile His Glu Asp Tyr Ala Val Ala Asn Val
210 215 220

Gly Thr Ser Gln Pro Gln Ser Pro Pro Thr Ser Ala Thr Glu Val Leu
225 230 235 240

Pro Ala Asn Met Thr Ser Arg Arg Leu Thr Trp Ser Phe Glu Arg Ile
245 250 255

Ala Lys Ile His Ser Asn Gly His Tyr Cys Leu Glu Val Arg Leu
260 265 270

<210> 61

<211> 1032

<212> DNA

<213> Salsola komarovii

<220>

<221> CDS

<222> (1).. (732)

<400> 61

cca caa cga aga ccc gac ccg gtc ccg aac ctt cac ggt cag ctt ttt 48
Pro Gln Arg Arg Pro Asp Pro Val Pro Asn Leu His Gly Gln Leu Phe
1 5 10 15

caa cac cga aat cca cac cac cgt gac ctc cac ccc tgc cgt agc ccg 96
Gln His Arg Asn Pro His His Arg Asp Leu His Pro Cys Arg Ser Pro
20 25 30

gca atg ggt cca ctc cct ccg cag act cat ctg cgc tgg tat tcc ctc 144
Ala Met Gly Pro Leu Pro Pro Gln Thr His Leu Arg Trp Tyr Ser Leu
35 40 45

tcg cgc tac tcc ccc gtg atc ggc ctc ggc gtc caa tgg aag ccc tcc 192
Ser Arg Tyr Ser Pro Val Ile Gly Leu Gly Val Gln Trp Lys Pro Ser
50 55 60

tcc acc tca gct gcc act ctt caa ctc agc atc gac aaa aag tgc ctc 240
Ser Thr Ser Ala Ala Thr Leu Gln Leu Ser Ile Asp Lys Lys Cys Leu
65 70 75 80

atc ttc caa ctc tcc cac tcc ccc gcc atc ccc gcc acc ctc cgc gac 288
Ile Phe Gln Leu Ser His Ser Pro Ala Ile Pro Ala Thr Leu Arg Asp
85 90 95

ctc ctc ctc gac gat cgc gtc acc ttc ttt ggt gtc cac aac ggc cgt 336
Leu Leu Leu Asp Asp Arg Val Thr Phe Phe Gly Val His Asn Gly Arg
100 105 110

gcc cgc gac ctc ctc caa ggg tcc cac cat gag ctc gac gtc aac aat 384
Ala Arg Asp Leu Leu Gln Gly Ser His His Glu Leu Asp Val Asn Asn

115	120	125	
ctg gtt gat ctt gcc gag gag gaa aat ggt cat tac ttg aag tgg tcc			432
Leu Val Asp Leu Ala Glu Glu Glu Asn Gly His Tyr Leu Lys Trp Ser			
130	135	140	
atg gaa gac atg gct gaa gat gtg ttg ggc ttt tgt ggg gta cac aaa			480
Met Glu Asp Met Ala Glu Asp Val Leu Gly Phe Cys Gly Val His Lys			
145	150	155	160
ccc agg aag gtt atg tta agt ggt tgg gat cag tat tgc ttg tct aat			528
Pro Arg Lys Val Met Leu Ser Gly Trp Asp Gln Tyr Cys Leu Ser Asn			
165	170	175	
gac cag gtt cag tat gct tgt gtt gat gct tac gtt tct ctt cgt ctt			576
Asp Gln Val Gln Tyr Ala Cys Val Asp Ala Tyr Val Ser Leu Arg Leu			
180	185	190	
gct cga gct tat ggg tac cac cgt ctc gat cac gat gat gat tat gat			624
Ala Arg Ala Tyr Gly Tyr His Arg Leu Asp His Asp Asp Asp Tyr Asp			
195	200	205	
gac cat gac gac gat gat aac gac cac acc gat gat gat tac gat gac			672
Asp His Asp Asp Asp Asp Asn Asp His Thr Asp Asp Asp Tyr Asp Asp			
210	215	220	
gtt tac gac cgc aat ata ggc tct gat gat gat ggt tat gat gcc gat			720
Val Tyr Asp Arg Asn Ile Gly Ser Asp Asp Asp Gly Tyr Asp Ala Asp			
225	230	235	240
gat gat cga cga tgatcaattt ggactagact tcgttattgg aagggtccga			772
Asp Asp Arg Arg			
tcatcatgcc agtctaatta caaagagaca agaaataaaa atgatgatca aaaaaagaag			832
tcaatccata tacgtaattt tcattgcaat atcaattttg aggtgtttta ttattgcct			892

gtaataatag ttttatttaa taatagcact atagatctca tcctaacctt tacttattgg 952

gcttatgcgc tgtatgtcca ataaccaagt ttaatttatt tcatgatctg atgattactg 1012

caaaaaaaaa aaaaaaaaaa 1032

<210> 62

<211> 244

<212> PRT

<213> Salsola komarovii

<400> 62

Pro Gln Arg Arg Pro Asp Pro Val Pro Asn Leu His Gly Gln Leu Phe
1 5 10 15

Gln His Arg Asn Pro His His Arg Asp Leu His Pro Cys Arg Ser Pro
20 25 30

Ala Met Gly Pro Leu Pro Pro Gln Thr His Leu Arg Trp Tyr Ser Leu
35 40 45

Ser Arg Tyr Ser Pro Val Ile Gly Leu Gly Val Gln Trp Lys Pro Ser
50 55 60

Ser Thr Ser Ala Ala Thr Leu Gln Leu Ser Ile Asp Lys Lys Cys Leu
65 70 75 80

Ile Phe Gln Leu Ser His Ser Pro Ala Ile Pro Ala Thr Leu Arg Asp
85 90 95

Leu Leu Leu Asp Asp Arg Val Thr Phe Phe Gly Val His Asn Gly Arg
100 105 110

Ala Arg Asp Leu Leu Gln Gly Ser His His Glu Leu Asp Val Asn Asn

115	120	125
Leu Val Asp Leu Ala Glu Glu Glu Asn Gly His Tyr Leu Lys Trp Ser		
130	135	140
Met Glu Asp Met Ala Glu Asp Val Leu Gly Phe Cys Gly Val His Lys		
145	150	155
Pro Arg Lys Val Met Leu Ser Gly Trp Asp Gln Tyr Cys Leu Ser Asn		
165	170	175
Asp Gln Val Gln Tyr Ala Cys Val Asp Ala Tyr Val Ser Leu Arg Leu		
180	185	190
Ala Arg Ala Tyr Gly Tyr His Arg Leu Asp His Asp Asp Asp Tyr Asp		
195	200	205
Asp His Asp Asp Asp Asp Asn Asp His Thr Asp Asp Asp Tyr Asp Asp		
210	215	220
Val Tyr Asp Arg Asn Ile Gly Ser Asp Asp Asp Gly Tyr Asp Ala Asp		
225	230	235
		240
Asp Asp Arg Arg		

<210> 63

<211> 1029

<212> DNA

<213> Mesembryanthemum crystallinum

<220>

<221> CDS

<222> (3).. (824)

<400> 63

ca cat atc agc cac atc cac tta att ccc cac agt ctt agt ctc tta 47

His Ile Ser His Ile His Leu Ile Pro His Ser Leu Ser Leu Leu

1 5 10 15

gac acc cat ctt agt ctt aag cct ctc atg gcc acc gcg gta ttc tca 95

Asp Thr His Leu Ser Leu Lys Pro Leu Met Ala Thr Ala Val Phe Ser

20 25 30

cct tct gcc ctt cta tcc acc tcc aca tcc acc tca aca acc cct ctt 143

Pro Ser Ala Leu Leu Ser Thr Ser Thr Ser Thr Ser Thr Thr Pro Leu

35 40 45

aaa gct ccc ccc ttg gcc tta acc aag acc cac gta acg atc cca tca 191

Lys Ala Pro Pro Leu Ala Leu Thr Lys Thr His Val Thr Ile Pro Ser

50 55 60

tca tca aag cca ccc cta acc aat tta act acc agt tta act gct gtc 239

Ser Ser Lys Pro Pro Leu Thr Asn Leu Thr Thr Ser Leu Thr Ala Val

65 70 75

gcc aca gct gct gcc ata atc ctg tcc aca acc cct cca tcg ttt gct 287

Ala Thr Ala Ala Ala Ile Ile Leu Ser Thr Thr Pro Pro Ser Phe Ala

80 85 90 95

gat gat ttg cag aca aat gca tac aac att tac tac ggc act gct gca 335

Asp Asp Leu Gln Thr Asn Ala Tyr Asn Ile Tyr Tyr Gly Thr Ala Ala

100 105 110

agt gca gcc aat tat gga ggc tac ggt ggc aat tcg aac aag aaa gat 383

Ser Ala Ala Asn Tyr Gly Gly Tyr Gly Gly Asn Ser Asn Lys Lys Asp

115 120 125

tca gct gag tac ata tat gac gtc cct gca ggt tgg aaa gag aga cta 431

Ser Ala Glu Tyr Ile Tyr Asp Val Pro Ala Gly Trp Lys Glu Arg Leu

130	135	140	
gta tca aaa gtt gag aag ggt acc aat gga aca gat agt gag ttc ttc			479
Val Ser Lys Val Glu Lys Gly Thr Asn Gly Thr Asp Ser Glu Phe Phe			
145	150	155	
aac ccc aag aag aag aca gag cga gag tac ctt acc tac ctt gct ggt			527
Asn Pro Lys Lys Lys Thr Glu Arg Glu Tyr Leu Thr Tyr Leu Ala Gly			
160	165	170	175
att agg caa cta ggt ccc aaa gaa gtg atc ctc aac aac tta gca ctc			575
Ile Arg Gln Leu Gly Pro Lys Glu Val Ile Leu Asn Asn Leu Ala Leu			
	180	185	190
tca gat gtg aac ctg caa gat caa att tcc agt gca gac tct gtg aca			623
Ser Asp Val Asn Leu Gln Asp Gln Ile Ser Ser Ala Asp Ser Val Thr			
	195	200	205
tca gaa gag agg aaa gat gac aag gga cag gtt tac tat gat tat gag			671
Ser Glu Glu Arg Lys Asp Asp Lys Gly Gln Val Tyr Tyr Asp Tyr Glu			
	210	215	220
att gct gga gct ggt tca cac agt ttg ata tcg gta aca tgt gcc agg			719
Ile Ala Gly Ala Gly Ser His Ser Leu Ile Ser Val Thr Cys Ala Arg			
	225	230	235
aac aag cta tat gcg cat ttt gtt agc gca cca aca ccc gaa tgg aat			767
Asn Lys Leu Tyr Ala His Phe Val Ser Ala Pro Thr Pro Glu Trp Asn			
240	245	250	255
cgg gat caa gat atg ctg agg cac atc cac aac tca ttt aca aca gtc			815
Arg Asp Gln Asp Met Leu Arg His Ile His Asn Ser Phe Thr Thr Val			
	260	265	270
ggg tca ttc tagaaagtgt atatgataat catttataga gatgtcagag			864
Gly Ser Phe			

aggcatacat ttgaatgtac ttctgatgag ctggacttct tgatctatgt aacattgtaa 924

cgaaaattct ttctgggtta tcagaaacct agtgagtgc tgaaacttgc aatgagaaac 984

tcttcaataa acaatgactt gtatcaaaaa aaaaaaaaaa aaaaa 1029

<210> 64

<211> 274

<212> PRT

<213> Mesembryanthemum crystallinum

<400> 64

His Ile Ser His Ile His Leu Ile Pro His Ser Leu Ser Leu Leu Asp
1 5 10 15

Thr His Leu Ser Leu Lys Pro Leu Met Ala Thr Ala Val Phe Ser Pro
20 25 30

Ser Ala Leu Leu Ser Thr Ser Thr Ser Thr Ser Thr Pro Leu Lys
35 40 45

Ala Pro Pro Leu Ala Leu Thr Lys Thr His Val Thr Ile Pro Ser Ser
50 55 60

Ser Lys Pro Pro Leu Thr Asn Leu Thr Thr Ser Leu Thr Ala Val Ala
65 70 75 80

Thr Ala Ala Ala Ile Ile Leu Ser Thr Thr Pro Pro Ser Phe Ala Asp
85 90 95

Asp Leu Gln Thr Asn Ala Tyr Asn Ile Tyr Tyr Gly Thr Ala Ala Ser
100 105 110

Ala Ala Asn Tyr Gly Gly Tyr Gly Gly Asn Ser Asn Lys Lys Asp Ser

115	120	125
Ala Glu Tyr Ile Tyr Asp Val Pro Ala Gly Trp Lys Glu Arg Leu Val		
130	135	140
Ser Lys Val Glu Lys Gly Thr Asn Gly Thr Asp Ser Glu Phe Phe Asn		
145	150	155
Pro Lys Lys Lys Thr Glu Arg Glu Tyr Leu Thr Tyr Leu Ala Gly Ile		
165	170	175
Arg Gln Leu Gly Pro Lys Glu Val Ile Leu Asn Asn Leu Ala Leu Ser		
180	185	190
Asp Val Asn Leu Gln Asp Gln Ile Ser Ser Ala Asp Ser Val Thr Ser		
195	200	205
Glu Glu Arg Lys Asp Asp Lys Gly Gln Val Tyr Tyr Asp Tyr Glu Ile		
210	215	220
Ala Gly Ala Gly Ser His Ser Leu Ile Ser Val Thr Cys Ala Arg Asn		
225	230	235
Lys Leu Tyr Ala His Phe Val Ser Ala Pro Thr Pro Glu Trp Asn Arg		
245	250	255
Asp Gln Asp Met Leu Arg His Ile His Asn Ser Phe Thr Thr Val Gly		
260	265	270
Ser Phe		

<210> 65

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 65

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33

<210> 66

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 66

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30

<210> 67

<211> 225

<212> DNA

<213> Bruguiera sexangula

<400> 67

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cctttcaagt tcacaaacce gtcgttactc actcgatcgc taagcttttc atcaaaaggt 120

tcaagctttg acagcttctc tgtacccaaa agatcttttt cttgcagaag ccaagccact 180

ccatctgatg atgcctcaag acccaccaaa gttcaagagc tgtaa 225

<210> 68
<211> 74
<212> PRT
<213> Bruguiera sexangula

<400> 68

Met Lys Val Val Gly Pro Ala Arg Ser Lys Ser Ala Thr Val Pro Thr
1 5 10 15

Gln Thr Val Leu Pro Phe Lys Phe Thr Asn Pro Ser Leu Leu Thr Arg
 20 25 30

Ser Leu Ser Phe Ser Ser Lys Gly Ser Ser Phe Asp Ser Phe Ser Val
 35 40 45

Pro Lys Arg Ser Phe Ser Cys Arg Ser Gln Ala Thr Pro Ser Asp Asp
 50 55 60

Ala Ser Arg Pro Thr Lys Val Gln Glu Leu
65 70

<210> 69
<211> 74
<212> PRT
<213> C-52

<400> 69

Met Lys Val Val Gly Pro Ala Arg Ser Lys Ser Ala Thr Val Pro Thr

1	5	10	15
Gln Thr Val Leu Pro Phe Lys Phe Thr Asn Pro Ser Leu Leu Thr Arg			
	20	25	30
Ser Leu Ser Phe Ser Ser Lys Gly Ser Ser Phe Asp Ser Phe Ser Val			
	35	40	45
Pro Lys Arg Ser Phe Ser Cys Arg Ser Gln Ala Thr Pro Ser Asp Asp			
	50	55	60
Ala Ser Arg Pro Thr Lys Val Gln Glu Leu			
65	70		

<210> 70
 <211> 225
 <212> DNA
 <213> Bruguiera sexangula

<400> 70
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 cctttcaagt tcacaaacce gtcgttactc actcgatcgc taagcttttc atcaaaaggt 120
 tcaagctttg acagcttctc tgtacccaaa agatcttttt cttgcagaag ccaagccacc 180
 ccattctgatg atgcctcaag acccaccaaa gttcaagagc tgtaa 225

<210> 71
 <211> 73

<212> PRT

<213> Bruguiera sexangula

<400> 71

Met Lys Val Val Gly Pro Ala Arg Ser Lys Ser Ala Thr Val Pro Thr
1 5 10 15

Gln Thr Val Leu Pro Phe Lys Phe Ala Asn Pro Ser Leu Leu Thr Arg
20 25 30

Ser Leu Ser Phe Ser Ser Lys Gly Ser Ser Phe Asp Ser Phe Ser Val
35 40 45

Pro Lys Arg Ser Phe Ser Cys Arg Ser Gln Ala Thr Pro Ser Asp Asp
50 55 60

Ala Ser Arg Pro Thr Lys Val Gln Glu
65 70

<210> 72

<211> 225

<212> DNA

<213> Bruguiera sexangula

<400> 72

atgaaggtgg tcggccctgc aagatcaaag agtgctactg taccaccca aacagtattg 60

cctttcaagt tcgcaaacc gtcgttactc actcgatcgc taagcttttc atcaaaaggt 120

tcaagctttg acagcttctc tgtacccaaa agatcttttt cttgcagaag ccaagccact 180

ccatctgatg atgcctcaag acccaccaaa gttcaagagc tgtaa

225